



P07741US01_6-19-06_Sequence.txt
SEQUENCE LISTING

<110> TRAMMEL, Magnus

<120> BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED PROTEINS FROM GRAM-POSITIVE BACTERIA

<130> P07741US01/BAS

<140> 10/661809

<141> 2003-09-15

<150> 60/410303

<151> 2002-09-13

<160> 57

<170> PatentIn version 3.1

<210> 1

<211> 5

<212> PRT

<213> Staphylococcus epidermidis

<220>

<221> MISC_FEATURE

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<210> 2

<211> 777

<212> PRT

<213> Staphylococcus epidermidis

<400> 2

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Gly Ala Ile Val Ser Ile Glu Lys Ala Glu Lys Asn Phe Val Ile Thr
20 25 30

Tyr Ala Ser Gly Lys Lys Ala Gln Ile Ser Ile Leu Asn Asp His Leu
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35

40

45

Phe Arg Tyr His Leu Asp Pro Thr Gly Lys Phe Glu Glu Tyr Pro Thr
50 55 60

Pro Asn Asp Pro Lys His Val Ala Lys Ile Thr Ala Lys Thr Met Ala
65 70 75 80

Asp Tyr Gly Thr Gln Ala Phe Glu Gln Thr Asn Val Thr Asp Ser Gly
85 90 95

Asn Gln Phe Ile Leu Glu Asn Asn Gly Leu Lys Ile Met Phe Glu Lys
100 105 110

Glu Ser Ala Leu Met Lys Val Leu Asp Lys Lys Lys Asn Gln Val Ile
115 120 125

Leu Glu Glu Thr Ala Pro Leu Ser Phe Lys Asn Asp Lys Ala Thr Gln
130 135 140

Thr Leu Lys Gln Ser Ser Gln Glu Asn Tyr Phe Gly Gly Gly Thr Gln
145 150 155 160

Asn Gly Arg Phe Thr His Lys Gly Thr Ala Ile Gln Ile Val Asn Thr
165 170 175

Asn Asn Trp Val Asp Gly Gly Val Ala Ser Pro Asn Pro Phe Tyr Trp
180 185 190

Ser Thr Ala Gly Tyr Gly Val Val Arg Asn Thr Trp Lys Pro Gly Asn
195 200 205

Tyr Asp Phe Gly Ser His Asp Pro Gln Lys Thr Thr Thr Thr His Glu
210 215 220

Gly Thr Asp Phe Asp Ala Phe Tyr Phe Phe Asn Asp Ser Ser Ala Gly
225 230 235 240

Ile Leu Lys Asp Tyr Tyr Glu Leu Thr Gly Lys Pro Ala Leu Met Pro
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245

250

255

Glu Tyr Gly Phe Tyr Glu Ala His Leu Asn Ala Tyr Asn Arg Asp Tyr
260 265 270

Trp Val Lys Val Ala Glu Gly Thr Ala Gly Ala Val Lys Phe Glu Asp
275 280 285

Gly Asn Phe Tyr Lys Glu Tyr Gln Pro Gly Asp Leu Gly Asn Leu Asn
290 295 300

Gly Thr Leu Glu Ser Leu Asn Gly Glu Lys Glu Asn Tyr Gln Phe Ser
305 310 315 320

Ala Arg Ala Val Ile Asp Arg Tyr Lys Lys Asn Asp Met Pro Leu Gly
325 330 335

Trp Phe Leu Pro Asn Asp Gly Tyr Gly Ala Gly Tyr Gly Gln Thr Asp
340 345 350

Ser Leu Asp Gly Asp Val Gln Asn Leu Lys Glu Phe Thr Glu Tyr Ala
355 360 365

Gln Ala Asn Gly Val Glu Val Gly Leu Trp Thr Gln Ser Asn Leu His
370 375 380

Pro Ala Asp Pro Lys Asn Pro Lys Lys Gly Glu Arg Asp Ile Ala Lys
385 390 395 400

Glu Val Ser Val Ala Gly Val Lys Ala Leu Lys Thr Asp Val Ala Trp
405 410 415

Val Gly Tyr Gly Tyr Ser Phe Gly Leu Asn Gly Val Glu Asp Ala Ala
420 425 430

Asn Val Phe Val Lys Glu Thr Asp Gly Ala Val Arg Pro Met Ile Val
435 440 445

Ser Leu Asp Gly Trp Ala Gly Thr Gln Arg His Ala Gly Ile Trp Thr
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450

455

460

Gly Asp Gln Thr Gly Gly Gln Trp Glu Tyr Ile Arg Phe His Ile Pro
465 470 475 480

Thr Tyr Ile Gly Thr Ser Leu Ser Gly Gln Pro Asn Val Gly Ser Asp
485 490 495

Met Asp Gly Ile Phe Gly Gly Lys Asn Lys Glu Ile Asn Ile Arg Asp
500 505 510

Phe Gln Trp Lys Thr Phe Thr Pro Val Gln Leu Asn Met Asp Gly Trp
515 520 525

Gly Ser Asn Pro Lys Thr Pro Phe Ala Phe Asp Gln Glu Ala Thr Asp
530 535 540

Leu Asn Arg Ala Tyr Leu Lys Leu Lys Ser Met Met Pro Tyr Asn
545 550 555 560

Tyr Ser Ile Ala Lys Glu Ser Val Asp Gly Leu Pro Met Val Arg Ala
565 570 575

Met Ala Leu Glu Phe Pro Asn Glu Gly Thr Ala Tyr Thr Lys Asp Ser
580 585 590

Gln Tyr Gln Tyr Met Trp Gly Pro Asn Leu Leu Val Ala Pro Ile Tyr
595 600 605

Asn Gly Asn Gln Asp Glu Ala Gly Asn Ser Ile Arg Asp Gly Ile Tyr
610 615 620

Leu Pro Asp Glu Lys Gln Val Trp Val Asp Leu Phe Thr Gly Glu Lys
625 630 635 640

Tyr Gln Gly Gly Arg Val Leu Asn Gly Val Lys Thr Pro Leu Trp Lys
645 650 655

Val Pro Val Phe Val Lys Asp Gly Ser Ile Ile Pro Met Thr Asn Pro
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660

665

670

Asn Asn Asn Pro Lys Glu Ile Gln Arg Asp Gln Arg Ser Phe Leu Ile
 675 680 685

Tyr Pro Asn Gly Thr Thr Ser Phe Asn Met Tyr Glu Asp Asp Gly Ile
 690 695 700

Ser Thr Ser Tyr Glu Ala Gly Gln Ser Ala Thr Thr Lys Ile Asn Ser
 705 710 715 720

Gln Gly Pro Lys Ser Asn Glu Lys Gly Asp Leu Thr Val Thr Ile Glu
 725 730 735

Pro Thr Lys Gly Ser Tyr Lys Asp Phe Val Asp Glu Arg Ser Thr Thr
 740 745 750

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Gly Gly Thr Glu Val Thr Leu Lys Gln
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<210> 3

<211> 1010

<212> PRT

<213> Staphylococcus epidermidis

<400> 3

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 20 25 30

Lys Leu Asn Gln Ser Ala Leu Ser Val Lys Leu Ala Lys Gln Ser Val
 35 40 45

Thr Ala Lys Asp Val Gln Ile Thr Val Lys Gly Phe Ile Asn Lys Gly
 50 55 60

P07741US01_6-19-06_Sequence.txt

Thr Val Asp Gly Gly Asn Thr Thr Val Asp Asp Gln Leu Thr Ile Pro
65 70 75 80

Ala Asn Val Ala Ile Asn Glu Glu Lys Thr Thr Pro Ser Ser Leu Thr
85 90 95

Leu Gln Trp Asp Gln Val Thr Glu Ala Thr Ser Tyr Glu Val Glu Arg
100 105 110

Asp Gly Thr Val Phe Gly Asn Ile Gln Thr Asn Thr Ala Thr Phe Asp
115 120 125

Gly Phe Ser Phe Leu Ser Glu His Thr Phe Arg Val Arg Ala Val Gly
130 135 140

Lys Asn Gly Val Ser Glu Trp Ser Glu Pro Ile Lys Gly Lys Thr Gln
145 150 155 160

Asp Asp Pro Tyr Lys Glu Thr Ile Asn Gln Val Lys Ala Thr Ser Asn
165 170 175

Leu Pro Glu Gln Pro Gly Ala Glu Leu Lys Lys Leu Thr Asp Lys Asp
180 185 190

Leu Ser Thr Gly Trp His Thr Asn Trp Ser Thr Gly Ile Ala Asn Pro
195 200 205

Ser Asp Gly Asn Phe Leu Ser Leu Lys Phe Asp Leu Gly Ala Glu Tyr
210 215 220

Gln Met Asp Lys Ile Glu Tyr Leu Pro Arg Asp Asn Ala Gly Asn Gly
225 230 235 240

Asn Ile Leu Gln Leu Gln Tyr Arg Thr Ser Lys Asp Gly Ala Asn Trp
245 250 255

Thr Glu Phe Ser Glu Pro Ile Asn Trp Lys Gln Asp Ala Leu Thr Lys
260 265 270

P07741US01_6-19-06_Sequence.txt

Thr Ile Glu Thr Lys Asp Gln Ala Tyr Arg Phe Val Glu Met Lys Val
275 280 285

Leu Lys Ser Val Gly Asn Phe Gly Ser Gly Arg Glu Met Leu Phe Tyr
290 295 300

Lys Gln Pro Gly Thr Glu Gly Ile Leu His Gly Asp Ile Thr Asn Asp
305 310 315 320

Gly Thr Ile Asp Glu Asn Asp Ala Met Ser Tyr Arg Asn Tyr Thr Gly
325 330 335

Leu Glu Ser Val Asp Ser Asp Phe Asn Gly Tyr Val Glu Lys Gly Asp
340 345 350

Leu Asn Lys Asn Gly Val Ile Asp Ala Tyr Asp Ile Ser Tyr Val Leu
355 360 365

Arg Gln Leu Asp Gly Gly Ile Glu Ile Pro Asp Val Glu Glu Ile Ala
370 375 380

Gly Gly Leu Ser Leu Ala Val Val Asn Glu Asn Gly Lys Asp Thr Tyr
385 390 395 400

Leu Pro Gly Asp Thr Leu Thr Phe Ile Leu Lys Gly Gln Asp Leu Lys
405 410 415

Asn Ile Asn Ala Leu Ser Thr Lys Met Ser Phe Asp Ser Ser Lys Phe
420 425 430

Glu Leu Val Gly Gln Pro Ala Thr Thr Asn Asn Thr Gln Gln Met Glu
435 440 445

Asn Tyr Ser Lys Tyr Arg Lys His Ser Asn Asp Val Glu Asn Leu Tyr
450 455 460

Leu Val Leu Ser Asn Gln Gly Asn Lys Gln Leu Leu Asn Gly Ser Met
465 470 475 480

P07741US01_6-19-06_Sequence.txt

Asp Leu Val Thr Phe Lys Val Lys Val Lys Glu Thr Thr Arg Val Lys
485 490 495

Arg Ala Thr Thr Val Glu Gln Pro Leu Gln Phe Asp Met Ser Gln Gly
500 505 510

Leu Leu Val Gly Gln Gly Phe Gln Gln Ala Thr Leu Ser Asp Phe Ser
515 520 525

Val Thr Val Lys Pro Thr Glu Leu Val Asp Lys Glu Leu Leu Gln Ala
530 535 540

Leu Ile Thr Leu Asn Gln Ala Arg Val Glu Lys Glu Tyr Thr Pro Glu
545 550 555 560

Thr Trp Ala Ile Phe Lys Pro Ile Leu Asp Glu Ala Val Ala Val Leu
565 570 575

Ala Asn Glu Gln Ala Thr Gln Thr Asp Val Ser Ala Ala Ala Glu Asn
580 585 590

Leu Glu Lys Ala Ala Ser Gln Leu Glu Lys Met Pro Asp Val Ala Asn
595 600 605

Lys Ala Asp Leu Glu Lys Ala Ile Gln Glu Gly Leu Ala Lys Lys Pro
610 615 620

Ser Asp Gly Gln Glu Phe Thr Glu Glu Thr Lys Lys Val Leu Glu Glu
625 630 635 640

Ser Leu Ala Ala Ala Gln Lys Val Phe Ala Gln Glu Lys Val Thr Gln
645 650 655

Glu Glu Ile Asp Gln Ala Thr Lys Thr Leu Arg Glu Ala Ile Ala Gln
660 665 670

Leu Lys Glu Gln Pro Val Ala Val Asp Lys Glu Thr Leu Lys Glu Gln
675 680 685

P07741US01_6-19-06_Sequence.txt

Ile Ala Gln Ala Arg Gly Arg Lys Pro Glu Glu Gly Tyr Gln Phe Thr
690 695 700

Lys Glu Thr Glu Lys Gln Leu Gln Glu Ala Ile Gln Ala Ala Glu Ala
705 710 715 720

Ile Val Ala Lys Glu Thr Ala Thr Lys Glu Glu Val Ser Glu Ala Leu
725 730 735

Asn Ala Leu Glu Thr Ala Met Ala Gln Leu Lys Glu Val Pro Leu Val
740 745 750

Asn Lys Asp Gln Leu Gln Glu Val Val Lys Arg Ala Gln Gln Val Thr
755 760 765

Pro Ser Glu Gly His Gln Phe Thr Ala Ser Ser Leu Gln Glu Leu Gln
770 775 780

Lys Ala Leu Leu Ala Ala Lys Asn Thr Leu Lys Asn Pro Ala Ala Asn
785 790 795 800

Gln Lys Met Ile Asp Glu Ala Val Ala Glu Leu Thr Ser Ala Ile Asp
805 810 815

Gly Leu Gln Glu Glu Val Leu Val Thr Asp Lys Lys Ala Leu Glu Ala
820 825 830

Met Ile Ala Lys Ala Lys Ala Ile Lys Pro Ser Ala Gly Lys Glu Phe
835 840 845

Thr Ser Glu Ser Lys Ala Arg Leu Thr Glu Ala Ile Asp Gln Ala Glu
850 855 860

Gly Ile Leu Ala Asp Lys Asn Ala Arg Gln Glu Gln Ile Asp Ile Ala
865 870 875 880

Glu Lys Asn Val Lys Thr Ala Leu Asp Ser Leu Glu Glu Gln Val Leu
885 890 895

P07741US01_6-19-06_Sequence.txt

Gln Thr Asp Lys Thr Lys Leu Lys Glu Leu Leu Gln Lys Ala Glu Thr
900 905 910

Leu Lys Pro Lys Ala Gly Lys Gln Phe Thr Lys Ala Ser Gln Glu Ala
915 920 925

Leu Ala Glu Ala Ile Lys Gln Ala Lys Ala Leu Val Glu Asp Pro Asn
930 935 940

Ala Thr Gln Glu Ala Val Asp Lys Cys Leu Ser Ile Leu Ser Gln Ala
945 950 955 960

Ile Glu Ala Met Ala Glu Glu Pro Ile Ser Ser Asn Ser Thr Gly Asn
965 970 975

Asn Gly Asn His Ser Thr Val Ser Gly Thr Gly Gly Val Thr Ser Gln
980 985 990

Gly Lys Gly Thr Ala Thr Gly Gly Thr Thr Thr Lys Thr Thr Thr Ser
995 1000 1005

Gly Thr
1010

<210> 4
<211> 1108
<212> PRT
<213> Staphylococcus epidermidis

<400> 4

Glu Glu Val Asn Ser Asp Gly Gln Leu Thr Leu Gly Glu Val Lys Gln
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20 25 30

Val Thr Gln Glu Val Val Val His Tyr Ser Ala Asn Val Ser Ile Lys
35 40 45

P07741US01_6-19-06_Sequence.txt

Ala Ala His Trp Ala Ala Pro Asn Asn Thr Arg Lys Ile Gln Val Asp
50 55 60

Asp Gln Lys Lys Gln Ile Gln Ile Glu Leu Asn Gln Gln Ala Leu Ala
65 70 75 80

Asp Thr Leu Val Leu Thr Leu Asn Pro Thr Ala Thr Glu Asp Val Thr
85 90 95

Phe Ser Tyr Gly Gln Gln Arg Ala Leu Thr Leu Lys Thr Gly Thr
100 105 110

Asp Pro Thr Glu Ser Thr Ala Ile Thr Ser Ser Pro Ala Ala Ser Ala
115 120 125

Asn Glu Gly Ser Thr Glu Glu Ala Ser Thr Asn Ser Ser Val Pro Arg
130 135 140

Ser Ser Glu Glu Thr Val Ala Ser Thr Thr Lys Ala Ile Glu Ser Lys
145 150 155 160

Thr Thr Glu Ser Thr Thr Val Lys Pro Arg Val Ala Gly Pro Thr Asp
165 170 175

Ile Ser Asp Tyr Phe Thr Gly Asp Glu Thr Thr Ile Ile Asp Asn Phe
180 185 190

Glu Asp Pro Ile Tyr Leu Asn Pro Asp Gly Thr Pro Ala Thr Pro Pro
195 200 205

Tyr Lys Glu Asp Val Thr Ile His Trp Asn Phe Asn Trp Ser Ile Pro
210 215 220

Glu Asp Val Arg Glu Gln Met Lys Ala Gly Asp Tyr Phe Glu Phe Gln
225 230 235 240

Leu Pro Gly Asn Leu Lys Pro Asn Lys Pro Gly Ser Gly Asp Leu Val
245 250 255

P07741US01_6-19-06_Sequence.txt

Asp Ala Glu Gly Asn Val Tyr Gly Thr Tyr Thr Ile Ser Glu Asp Gly
260 265 270

Thr Val Arg Phe Thr Phe Asn Glu Arg Ile Thr Ser Glu Ser Asp Ile
275 280 285

His Gly Asp Phe Ser Leu Asp Thr His Leu Asn Asp Ser Asp Gly Arg
290 295 300

Gly Pro Gly Asp Trp Val Ile Asp Ile Pro Thr Gln Glu Asp Leu Pro
305 310 315 320

Pro Val Val Ile Pro Ile Val Pro Asp Thr Glu Gln Gln Ile Asp Lys
325 330 335

Gln Gly His Phe Asp Arg Thr Pro Asn Pro Ser Ala Ile Thr Trp Thr
340 345 350

Val Asp Ile Asn Gln Ala Met Lys Asp Gln Thr Asn Pro Thr Val Thr
355 360 365

Glu Thr Trp Pro Thr Gly Asn Thr Phe Lys Ser Val Lys Val Tyr Glu
370 375 380

Leu Val Met Asn Leu Asp Gly Thr Ile Lys Glu Val Gly Arg Glu Leu
385 390 395 400

Ser Pro Asp Glu Tyr Thr Val Asp Lys Asn Gly Asn Val Thr Ile Lys
405 410 415

Gly Asp Thr Asn Lys Ala Tyr Arg Leu Glu Tyr Gln Thr Thr Ile Asp
420 425 430

Glu Ala Val Ile Pro Asp Gly Gly Asp Val Pro Phe Lys Asn His
435 440 445

Ala Thr Leu Thr Ser Asp Asn Asn Pro Asn Gly Leu Asp Ala Glu Ala
450 455 460

P07741US01_6-19-06_Sequence.txt

Thr Val Thr Ala Thr Tyr Gly Lys Met Leu Asp Lys Arg Asn Ile Asp
465 470 475 480

Tyr Asp Glu Ala Asn Gln Glu Phe Thr Trp Glu Ile Asn Tyr Asn Tyr
485 490 495

Gly Glu Gln Thr Ile Pro Lys Asp Gln Ala Val Ile Thr Asp Thr Met
500 505 510

Gly Asp Asn Leu Thr Phe Glu Pro Asp Ser Leu His Leu Tyr Ser Val
515 520 525

Thr Phe Asp Asp Lys Gly Asn Glu Val Val Gly Ala Glu Leu Val Glu
530 535 540

Gly Lys Asp Tyr Lys Val Val Ile Asn Gly Asp Gly Ser Phe Ala Ile
545 550 555 560

Asp Phe Leu His Asp Val Thr Gly Ala Val Lys Ile Asp Tyr Lys Thr
565 570 575

Lys Val Asp Gly Ile Val Glu Gly Asp Val Ala Val Asn Asn Arg Val
580 585 590

Asp Val Gly Thr Gly Gln His Ser Glu Asp Asp Gly Thr Ala Ser Gln
595 600 605

Gln Asn Ile Ile Lys Asn Thr Gly Ala Val Asp Tyr Gln Asn Ser Thr
610 615 620

Ile Gly Trp Thr Leu Ala Val Asn Gln Asn Asn Tyr Leu Met Glu Asn
625 630 635 640

Ala Val Ile Thr Asp Thr Tyr Glu Pro Val Pro Gly Leu Thr Met Val
645 650 655

Pro Asn Ser Leu Val Val Lys Asp Thr Thr Gly Ala Gln Leu Thr
660 665 670

P07741US01_6-19-06_Sequence.txt

Leu Gly Lys Asp Phe Met Val Glu Ile Thr Arg Asn Ala Asp Gly Glu
675 680 685

Thr Gly Phe Lys Val Ser Phe Ile Gly Ala Tyr Ala Lys Thr Ser Asp
690 695 700

Ala Phe His Ile Thr Tyr Thr Phe Phe Asp Val Thr Glu Leu Asp
705 710 715 720

Ala Asn Asn Pro Ala Leu Asp His Tyr Arg Asn Thr Ala Ala Ile Asp
725 730 735

Trp Thr Asp Glu Ala Gly Asn Asn His His Ser Glu Asp Ser Lys Pro
740 745 750

Phe Lys Pro Leu Pro Ala Phe Asp Leu Asn Ala Gln Lys Ser Gly Val
755 760 765

Tyr Asn Ala Val Thr Lys Glu Ile Thr Trp Thr Ile Ala Val Asn Leu
770 775 780

Ser Asn Asn Arg Leu Val Asp Ala Phe Leu Thr Asp Pro Ile Leu Thr
785 790 795 800

Asn Gln Thr Tyr Leu Ala Gly Ser Leu Lys Val Tyr Glu Gly Asn Thr
805 810 815

Lys Pro Asp Gly Ser Val Glu Lys Val Lys Pro Thr Gln Pro Leu Thr
820 825 830

Asp Ile Thr Met Glu Glu Pro Ser Glu Lys Asn Gln Asn Thr Trp Arg
835 840 845

Val Asp Phe Pro Asn Asp Ser Arg Thr Tyr Val Ile Glu Phe Lys Thr
850 855 860

Ser Val Asp Glu Lys Val Ile Glu Gly Ser Ala Ser Tyr Asp Asn Thr
865 870 875 880

P07741US01_6-19-06_Sequence.txt

Ala Ser Tyr Thr Asn Gln Gly Ser Ser Arg Asp Val Thr Gly Lys Val
885 890 895

Ser Ile Gln His Gly Gly Glu Ser Val Lys Lys Gly Gly Glu Tyr His
900 905 910

Lys Asp Asp Pro Asp His Val Tyr Trp His Val Met Ile Asn Gly Ala
915 920 925

Gln Ser Val Leu Asp Asp Val Val Ile Thr Asp Thr Pro Ser Pro Asn
930 935 940

Gln Val Leu Asp Pro Glu Ser Leu Val Ile Tyr Gly Thr Asn Val Thr
945 950 955 960

Glu Asp Gly Thr Ile Thr Pro Asp Lys Ser Val Ile Leu Glu Glu Gly
965 970 975

Lys Asp Tyr Thr Leu Glu Val Thr Thr Asp Asn Glu Thr Gly Gln Gln
980 985 990

Lys Ile Val Val Lys Met Ala His Ile Glu Ala Pro Tyr Tyr Met Glu
995 1000 1005

Tyr Arg Ser Leu Val Thr Ser Ser Ala Ala Gly Ser Thr Asp Thr
1010 1015 1020

Val Ser Asn Gln Val Ser Ile Thr Gly Asn Gly Ser Glu Val Val
1025 1030 1035

His Gly Asp Asp Asn Gly Asp Val Val Val Asp Ile Asp His Ser
1040 1045 1050

Gly Gly His Ala Thr Gly Thr Lys Gly Lys Ile Gln Leu Lys Lys
1055 1060 1065

Thr Ala Met Asp Glu Thr Thr Ile Leu Ala Gly Ala His Phe Gln
1070 1075 1080

P07741US01_6-19-06_Sequence.txt

Ile Trp Asp Gln Ala Lys Thr Gln Val Leu Arg Glu Gly Thr Val
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Asp Ala Thr Gly Val Ile Thr Phe Gly Gly
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<210> 5

<211> 999

<212> PRT

<213> Staphylococcus epidermidis

<400> 5

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Gly Glu Lys Ala Val Asp Gly Asp Glu Thr Thr Arg Trp Ser Ala Asp
35 40 45

Lys Gln Asp Glu Gln Trp Leu Ile Val Asp Leu Gly Glu Val Lys Asn
50 55 60

Ile Gly Glu Leu Val Leu Gln Leu His Ala Glu Ser Pro Val Tyr Glu
65 70 75 80

Ile Leu Val Ser Thr Asp Gly Glu Ser Tyr Gln Ser Ile Phe Lys Glu
85 90 95

Glu Asn Gly Lys Gly Gln Pro Thr Lys Lys Tyr Ile Asp Gly Asn
100 105 110

Asn Val Gln Ala Arg Phe Val Lys Tyr Gln Gln Met Lys Met Trp Gln
115 120 125

His Thr Asn Lys Gln Phe Tyr Ser Ser Ser Ile Ile Ser Phe Glu Ala
130 135 140

P07741US01_6-19-06_Sequence.txt

Tyr Glu Lys Lys Arg Leu Pro Glu Ala Ile Lys Leu Leu Thr Glu Asn
145 150 155 160

Leu Thr Ile Ser Glu Lys Arg Lys Gln Gln Leu Ala Phe Glu Val Ser
165 170 175

Pro Ala Gly Val Asp Ile Thr Glu Asp Gln Ile Glu Trp Ser Ser Ser
180 185 190

Asp Pro Thr Ile Val Thr Val Asp Gln Thr Gly Asn Leu Thr Ala Val
195 200 205

Lys Ser Gly Glu Ala Lys Val Thr Val Lys Ile Lys Gly Thr Glu Ile
210 215 220

Ser Asp Thr Ile Pro Val Thr Val Val Ala Glu Asn Lys Gln Tyr Ala
225 230 235 240

Glu Met Arg Ala Lys Trp Lys Met Arg Leu Leu Gly Thr Thr Gln Tyr
245 250 255

Asp Asn Asp Ala Asp Val Gln Gln Tyr Arg Ala Gln Ile Ala Thr Glu
260 265 270

Ser Leu Ala Leu Trp Gln Thr Leu Asn Gln Ala Ala Asp Arg Glu Tyr
275 280 285

Leu Trp Glu Arg Lys Pro Ser Asp Thr Val Ser Ala Asp Tyr Thr Thr
290 295 300

Gln Phe Thr Asn Ile Lys Lys Leu Ala Leu Gly Tyr Tyr Glu Pro Ser
305 310 315 320

Ser Glu Leu Phe Glu Lys Pro Glu Val Tyr Asp Ala Ile Val Lys Gly
325 330 335

Ile Glu Phe Met Ile Asp Thr Lys Lys Tyr Asn Gly Thr Tyr Tyr Thr
340 345 350

P07741US01_6-19-06_Sequence.txt

Gly Asn Trp Trp Asp Trp Gln Ile Gly Ser Ala Gln Pro Leu Thr Asp
355 360 365

Thr Leu Ile Leu Leu His Asp Asp Leu Leu Asn Thr Asp Ala Glu Lys
370 375 380

Leu Asn Lys Phe Thr Ala Pro Leu Met Leu Tyr Ala Lys Asp Pro Asn
385 390 395 400

Ile Gln Trp Pro Ile Tyr Arg Ala Thr Gly Ala Asn Leu Thr Asp Ile
405 410 415

Ser Ile Thr Val Leu Gly Thr Gly Leu Leu Leu Glu Asp Asn Gln Arg
420 425 430

Leu Val Gln Val Gln Glu Ala Val Pro Ser Val Leu Lys Ser Val Ser
435 440 445

Ser Gly Asp Gly Leu Tyr Pro Asp Gly Ser Leu Ile Gln His Gly Tyr
450 455 460

Phe Pro Tyr Asn Gly Ser Tyr Gly Asn Glu Leu Leu Lys Gly Phe Gly
465 470 475 480

Arg Ile Gln Thr Ile Leu Gln Gly Ser Asp Trp Glu Met Asn Asp Pro
485 490 495

Asn Ile Ser Asn Leu Phe Asn Val Val Asp Lys Gly Tyr Leu Gln Leu
500 505 510

Met Val Asn Gly Lys Met Pro Ser Met Val Ser Gly Arg Ser Ile Ser
515 520 525

Arg Ala Pro Glu Thr Asn Pro Phe Thr Thr Glu Phe Glu Ser Gly Lys
530 535 540

Glu Thr Ile Ala Asn Leu Thr Leu Ile Ala Lys Phe Ala Pro Glu Asn
545 550 555 560

P07741US01_6-19-06_Sequence.txt

Leu Arg Asn Asp Ile Tyr Thr Ser Ile Gln Thr Trp Leu Gln Gln Ser
565 570 575

Gly Ser Tyr Tyr His Phe Phe Lys Lys Pro Arg Asp Phe Glu Ala Leu
580 585 590

Ile Asp Leu Lys Asn Val Val Asn Ser Ala Ser Pro Ala Gln Ala Thr
595 600 605

Pro Met Gln Ser Leu Asn Val Tyr Gly Ser Met Asp Arg Val Leu Gln
610 615 620

Lys Asn Asn Glu Tyr Ala Val Gly Ile Ser Met Tyr Ser Gln Arg Val
625 630 635 640

Gly Asn Tyr Glu Phe Gly Asn Thr Glu Asn Lys Lys Gly Trp His Thr
645 650 655

Ala Asp Gly Met Leu Tyr Leu Tyr Asn Gln Asp Phe Ala Gln Phe Asp
660 665 670

Glu Gly Tyr Trp Ala Thr Ile Asp Pro Tyr Arg Leu Pro Gly Thr Thr
675 680 685

Val Asp Thr Arg Glu Leu Ala Asn Gly Ala Tyr Thr Gly Lys Arg Ser
690 695 700

Pro Gln Ser Trp Val Gly Gly Ser Asn Asn Gly Gln Val Ala Ser Ile
705 710 715 720

Gly Met Phe Leu Asp Lys Ser Asn Glu Gly Met Asn Leu Val Ala Lys
725 730 735

Lys Ser Trp Phe Leu Leu Asp Gly Gln Ile Ile Asn Leu Gly Ser Gly
740 745 750

Ile Thr Gly Thr Thr Asp Ala Ser Ile Glu Thr Ile Leu Asp Asn Arg
755 760 765

P07741US01_6-19-06_Sequence.txt

Met Ile His Pro Gln Glu Val Lys Leu Asn Gln Gly Ser Asp Lys Asp
770 775 780

Asn Ser Trp Ile Ser Leu Ser Ala Ala Asn Pro Leu Asn Asn Ile Gly
785 790 795 800

Tyr Val Phe Pro Asn Ser Met Asn Thr Leu Asp Val Gln Ile Glu Glu
805 810 815

Arg Ser Gly Arg Tyr Gly Asp Ile Asn Glu Tyr Phe Val Asn Asp Lys
820 825 830

Thr Tyr Thr Asn Thr Phe Ala Lys Ile Ser Lys Asn Tyr Gly Lys Thr
835 840 845

Val Glu Asn Gly Thr Tyr Glu Tyr Leu Thr Val Val Gly Lys Thr Asn
850 855 860

Glu Glu Ile Ala Ala Leu Ser Lys Asn Lys Gly Tyr Thr Val Leu Glu
865 870 875 880

Asn Thr Ala Asn Leu Gln Ala Ile Glu Ala Gly Asn Tyr Val Met Met
885 890 895

Asn Thr Trp Asn Asn Asp Gln Glu Ile Ala Gly Leu Tyr Ala Tyr Asp
900 905 910

Pro Met Ser Val Ile Ser Glu Lys Ile Asp Asn Gly Val Tyr Arg Leu
915 920 925

Thr Leu Ala Asn Pro Leu Gln Asn Asn Ala Ser Val Ser Ile Glu Phe
930 935 940

Asp Lys Gly Ile Leu Glu Val Val Ala Ala Asp Pro Glu Ile Ser Val
945 950 955 960

Asp Gln Asn Ile Ile Thr Leu Asn Ser Ala Gly Leu Asn Gly Ser Ser
965 970 975

P07741US01_6-19-06_Sequence.txt

Arg Ser Ile Ile Val Lys Thr Thr Pro Glu Val Thr Lys Glu Ala Leu
980 985 990

Glu Lys Leu Ile Gln Glu Gln
995

<210> 6

<211> 741

<212> PRT

<213> Staphylococcus epidermidis

<400> 6

Gln Glu Val Thr Ser Asp Ala Glu Lys Thr Val Glu Lys Asp Gly Leu
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20 25 30

Thr Val Thr Tyr Glu Val Thr Asn Thr Arg Asp Val Pro Ile Lys Asp
35 40 45

Leu Ile Leu Lys Gln Lys Asn Thr Asn Asp Ser Pro Ile Lys Phe Val
50 55 60

Leu Asp Thr Leu Ser Glu Glu Arg Gly Pro Thr Ser Leu Glu Glu Gln
65 70 75 80

Ala Lys Val Glu Thr Asn Glu Lys Asp Gln Thr Thr Asp Ile Lys Leu
85 90 95

Leu Asn Leu Gln Pro Asn Ser Thr Arg Lys Ile Thr Ile Asn Gly Gln
100 105 110

Ile Thr Thr Lys Ala Ser Asn Lys Leu Leu Val Ser Val Leu Ile Glu
115 120 125

Asp Asn Glu Lys Gly Thr Leu Val Ile Asp Leu Pro Ser Lys Asp Ile
130 135 140

Leu Ala Asp Lys Glu Ser Val Ser Lys Glu Lys Gln Glu Thr Ser Glu
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145

150

155

160

Thr Lys Val Glu Asn Gln Ala Asn Glu Thr Ala Ser Ser Thr Asn Glu
165 170 175

Met Thr Ala Thr Thr Ser Asn Glu Thr Lys Pro Glu Ala Gly Lys Ala
180 185 190

Ile Glu Ser Ile Gln Glu Thr Ala Leu Thr Gln Ala Thr Glu Ser Pro
195 200 205

Glu Gln Pro Pro Leu Lys Ala Gln Pro Thr Gly Pro Leu Val Pro Pro
210 215 220

Thr Pro Gly Arg Gly Phe Asn Thr Pro Ile Tyr Gln Ser Val His Lys
225 230 235 240

Gly Glu Leu Phe Ser Thr Gly Asn Thr Asn Leu Lys Ile Ala Asn Glu
245 250 255

Asn Thr Ala Ala Ala Gln Thr Phe Leu Asn Thr Arg Gly Ala Ser Ser
260 265 270

Gly Tyr Ala Ile Asn Asn Phe Pro Leu Glu Phe Ala Asp Val Asp Asn
275 280 285

Asp Pro Asn Thr Tyr Asn Ser Ser Arg Ala Tyr Ile Asp Leu Asn Gly
290 295 300

Ala Lys Glu Ile Ala Trp Ala Gly Leu Phe Trp Ser Ala Ser Arg Tyr
305 310 315 320

Lys Gly Pro Ala Tyr Gly Thr Asn Leu Ser Asp Glu Glu Ile Ser Ala
325 330 335

Pro Val Gln Phe Thr Thr Pro Asn Gly Thr Val Gln Arg Val Ser Pro
340 345 350

Gln Arg Tyr His Arg Ile Asp Gln Asp Ala Thr Asn Pro Gly Gln Arg
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P07741US01_6-19-06_Sequence.txt

355

360

365

Phe Gly Tyr Asn Asn Thr Gly Phe Ser Asn Tyr Ala Asp Val Thr Ser
 370 375 380

Ile Leu Gln Gly Asp Lys Ser Ala Thr Gly Ser Tyr Thr Leu Ala Asp
 385 390 395 400

Ile Pro Met Thr Ser Ser Leu Asn Gly Gln Tyr Gln Tyr Tyr Asn Phe
 405 410 415

Ser Gly Trp Ser Leu Phe Val Val Thr Lys Asp Gln Ala Ser Lys Ser
 420 425 430

Arg Ala Phe Ser Ile Tyr Tyr Gly Ala Arg Gly Asn Ala Ala Gly Thr
 435 440 445

Asn Asn Glu Phe Thr Met Ser Asn Phe Leu Thr Ala Lys Gln Gly Asn
 450 455 460

Leu Asp Pro Ile Val Thr Trp Phe Thr Val Gln Gly Asp Lys Tyr Trp
 465 470 475 480

Thr Gly Asp Asn Ala Gln Ile Lys Asn Ser Ala Gly Thr Trp Val Asn
 485 490 495

Ile Ser Asn Thr Leu Asn Pro Val Asn Asn Ala Met Asn Ala Thr Val
 500 505 510

Thr Asp Asn Asp Glu His Met Val Asp Lys Tyr Pro Gly Lys Phe Ala
 515 520 525

Pro Asp His Pro Asn Phe Leu Asp Ile Asp Ile Asp Arg Met Ala Ile
 530 535 540

Pro Glu Gly Val Leu Asn Ala Gly Gln Asn Gln Ile Asn Phe Arg Thr
 545 550 555 560

Thr Ser Ser Gly Asp Asp Tyr Ser Thr Asn Ala Ile Gly Phe Ala Val

P07741US01_6-19-06_Sequence.txt

565

570

575

Asn Ala Glu Thr Pro Glu Phe Glu Ile Lys Lys Glu Ile Val Glu Pro
580 585 590

Lys Glu Thr Tyr Lys Val Gly Glu Thr Ile Thr Tyr Arg Val Ser Leu
595 600 605

Lys Asn Thr Lys Ala Asp Ser Glu Ala Ile Asn Ser Val Ser Lys Asp
610 615 620

Ala Leu Asp Gly Arg Leu Asn Tyr Leu Pro Gly Ser Leu Lys Ile Ile
625 630 635 640

Ser Gly Pro Asn Ser Gly Glu Lys Thr Asp Ala Ser Gly Asp Asp Gln
645 650 655

Ala Glu Tyr Asp Glu Thr Asn Lys Gln Ile Ile val Arg Val Gly Asn
660 665 670

Gly Ala Thr Ala Thr Gln Gly Gly Ser Tyr Lys Ala Asp Thr Ala Glu
675 680 685

Thr Ile Tyr Glu Phe Lys Ala Arg Ile Asn Glu Arg Ala Lys Ala Asn
690 695 700

Glu Leu Val Pro Asn Ser Ala Thr Val Glu Ala Val Asp Ile Leu Thr
705 710 715 720

Ser Ala Lys Val Asn Glu Thr Ser Asn Ile Val Glu Ala Lys Ile Ala
725 730 735

Asp Glu Gln Val Thr
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<210> 7

<211> 570

<212> PRT

<213> Staphylococcus epidermidis

P07741US01_6-19-06_Sequence.txt

<400> 7

Glu Thr Gly Tyr Ala Gln Thr Glu Pro Thr Ser Thr Ser Glu Thr Asn
1 5 10 15

Gln Ile Ser Ala Thr Pro Asn Val Val Pro Arg Lys Gln Val Gly Asn
20 25 30

Ile Val Thr Ala Ile Gln Leu Thr Asp Lys Glu Gly Asn Pro Leu Gly
35 40 45

Thr Ile Asn Gln Tyr Thr Asp Ile Tyr Leu Arg Ile Glu Phe Asn Leu
50 55 60

Pro Asp Asn Thr Val Asn Ser Gly Asp Thr Ser Val Ile Thr Leu Pro
65 70 75 80

Glu Glu Leu Arg Leu Glu Lys Asn Met Thr Phe Asn Val Val Asp Asp
85 90 95

Thr Gly Thr Val Val Ala Ile Ala Gln Thr Asp Val Ala Asn Lys Thr
100 105 110

Val Thr Leu Thr Tyr Thr Asp Tyr Val Glu Asn His Ala Asn Ile Ser
115 120 125

Gly Ser Leu Tyr Phe Thr Ser Leu Ile Asp Phe Glu Asn Val Glu Asn
130 135 140

Glu Ser Lys Ile Pro Ile Tyr Val Thr Val Glu Gly Glu Lys Ile Phe
145 150 155 160

Ala Gly Asp Leu Asp Tyr Gln Gly Glu Gly Asp Asp Val Asn Glu Lys
165 170 175

Phe Ser Lys Tyr Ser Trp Phe Ile Glu Asp Asp Pro Thr Glu Ile Tyr
180 185 190

Asn Val Leu Arg Ile Asn Pro Thr Gly Gln Thr Tyr Thr Asp Leu Glu
195 200 205

P07741US01_6-19-06_Sequence.txt

Val Glu Asp Val Leu Lys Thr Glu Ser Leu Ser Tyr Met Lys Asp Thr
210 215 220

Met Lys Ile Glu Arg Gly Gln Trp Thr Leu Asp Gly Asn Ala Ile Trp
225 230 235 240

Gln Phe Thr Pro Glu Glu Asp Ile Thr Asp Gln Leu Ala Val Gln Tyr
245 250 255

Gly Pro Asp Asp Arg Asn Phe Ser Val His Phe Gly Asn Ile Gly Thr
260 265 270

Asn Glu Tyr Arg Ile Thr Tyr Lys Thr Lys Ile Asp His Leu Pro Glu
275 280 285

Lys Gly Glu Thr Phe Thr Asn Tyr Ala Lys Leu Thr Glu Asn Gln Thr
290 295 300

Val Val Glu Glu Val Glu Val Ser Arg Val Ser Gln Thr Gly Gly Gly
305 310 315 320

Glu Ala Asn Gly Glu Gln Tyr Val Val Glu Ile His Lys Glu Asp Glu
325 330 335

Ala Gly Gln Arg Leu Ala Gly Ala Glu Phe Glu Leu Ile Arg Asn Ser
340 345 350

Thr Asn Gln Thr Val Ala Lys Ile Thr Thr Asp Gln Asn Gly Thr Ala
355 360 365

Ile Val Lys Gly Leu Leu Lys Asp Asn Tyr Thr Leu Val Glu Thr Lys
370 375 380

Ala Pro Thr Gly Tyr Gln Leu Ser Gln Asn Lys Ile Pro Ile Thr Pro
385 390 395 400

Glu Asp Phe Gly Lys Asn Leu Val Ala Leu Lys Thr Val Val Asn His
405 410 415

P07741US01_6-19-06_Sequence.txt

Lys Ile Ser Tyr Gln Pro Val Ala Ala Ser Phe Leu Ala Gly Lys Val
420 425 430

Leu Leu Gly Lys Pro Leu Lys Asp Ala Glu Phe Gln Phe Glu Leu Leu
435 440 445

Asp Glu Lys Gly Thr Val Leu Glu Thr Val Ser Asn Asp Thr Leu Gly
450 455 460

Lys Ile Gln Phe Ser Pro Leu Thr Phe Glu Thr Pro Gly Asn Tyr Gln
465 470 475 480

Tyr Thr Ile Arg Glu Val Asn Thr Gln Gln Thr Gly Val Ser Tyr Asp
485 490 495

Thr His Asn Leu Gln Val Gln Val Thr Val Glu Ala Leu Leu Gly Asn
500 505 510

Leu Val Ala Thr Thr Gln Tyr Asp Gly Gly Gln Val Phe Thr Asn His
515 520 525

Tyr Thr Pro Glu Lys Pro Ile Glu Ser Thr Thr Pro Pro Thr Ser Gly
530 535 540

Thr Thr Asp Thr Thr Thr Asn Ser Thr Thr Glu Thr Thr Ser Ile Thr
545 550 555 560

Ile Glu Lys Gln Ala Ile Arg Asn Lys Glu
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<210> 8

<211> 3309

<212> DNA

<213> Staphylococcus epidermidis

<400> 8

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60

acagagcagc cattacaacg agaaattcaa ttgaaaaatg cacagttcat ggatactgct

P07741US01_6-19-06_Sequence.txt

120

gtaattgaaa aagacggata ttcttaccaa gtgactaatg gtacgcttta tctgactttg
180

gacgcacaag taaaaaagcc ggtacagctt tcgttagctg ttgagcaaag ttcgcttcaa
240

acagctcagc cacctaagtt attgtatgaa aacaacgaat atgatgttgc agttacttct
300

gaaaaaataa cagtagagga ttctgctaaa gaatcaactg aaccagaaaa aataactgta
360

ccagaaaata cgaaagaaac taacaaaaat gattcggtc cagaaaaaac agaacagccg
420

accgcaacag aagaggtaac caatccattt gcagaagcaa gaatggcgcc agtactttg
480

agagcgaatc tggcactgcc tttaattgca ccacaataca cgacggataa ttctggact
540

tatccgacag ctaattggca gcccacaggc aatcaaaatg tgttaaacca tcaaggaaat
600

aaagacggta gtgcacaatg ggacggccaa acgagttgga atggggaccc tactaatcgc
660

acaattctt atattgagta tggcggtaca ggagaccaag ccgattatgc catccaaaaa
720

tatgctagag aaacaacaac accaggcattt tttgatgtat atcttaatgt gcgtggaaat
780

gttcagaaag aaatcacgccc attggatttg gtcttagtgc ttgactggc cggtagtatg
840

aatgaaaaca atcggattgg tgaagttcaa aaaggagtga accgtttgt tgatacattg
900

gcagatagcg gtattaccaa taacatcaac atggctatg ttggctactc aagtgacggt
960

tataataaca acgccattca aatggggccg tttgatacag tcaaaaatcc aattaaaaat
1020

attacgcca a gtagcactag aggaggaact ttcactcaa aagcattaag agatgctgg
1080

gatatgttag caacgcca a tggacataag aaagtcatgg tacttttaac ggatggcg
1140

P07741US01_6-19-06_Sequence.txt

ccaacaccttct cttataaaagt gagtcgagtt caaacagagg cgatggtcg ctttacggg
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1260
aatgcgccag atcaaaaacaa tatcaataaa cgattaca gtacgtttat cgccacgata
1320
ggtggggcaa tggcttaaa acaacgtggg attgaaatac atggattggg cattcaattg
1380
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ggcctgttc agttcaaac attaccagaa gtgtcgctaa caggcgctac aattaatagt
1680
aatgagattt atttggtaa agggcaagaa attcaaattc attatcaagt acgtattcaa
1740
acagagtcag aaaacttcaa acctgattt tggtatcaa tgaatggtcg gacaacgtt
1800
cagccattag ccacggcccc tgaaaaagtt gatTTgggg ttccttcggg aaaagcacct
1860
ggcgtgaagt taaacgtgaa aaaaatctgg gaagagtatg atcaagaccc gacaagtcgg
1920
ccagataatg tgatttatga aatttagtaga aagcaagtaa ctgacacagc caactggcaa
1980
actgggtata ttaaattatc aaaaccagaa aatgatacca gcaatagttg ggagcgcaaa
2040
aatgtAACCC aacttccaa aaccgcggat gaaagctatc aagaagttct tggcttc
2100
caatacaaca atcaaggaca agctttcaat tatcaaacaa cccgtgaatt agcagttc
2160

P07741US01_6-19-06_Sequence.txt

ggttacagtc aagaaaaaat cgacgatact acttggaaaa acacgaagca gttcaagcca
2220

ttagatttaa aagtaatcaa aaattcttcc tcaggtgaga aaaacttagt gggagccgtc
2280

tttgaattga gtggtaaaaa tttcaaaaca acattagtgg acaataaaga tgtagctat
2340

tccttgccaa aagatgtgcg cctacaaaaa ggggaacgct atacattaac tgaagtaaaa
2400

gcacctgcag gacatgagtt aggcaagaaa acgacttggc aaattgaggt gagtgagcaa
2460

ggcaaagtaa gcatcgatgg acaagaagtg accaccacaa atcaagttat tccattggaa
2520

attgaaaata aattttcttc tttgccaatc agaatttagaa aatacaccat gcaaaatggc
2580

aaacaagtga acttagcaga ggactttt gcgttgc当地 gaaaaatgc tcaaggaagt
2640

taccaaactg tggcaactca aaaaacagat actacaggat tgagctattt taaaattagt
2700

gaacctggtg agtatcgaaat ggttggacaa tcaggaccat taggctacga cactttgt
2760

ggaaattatg aatttactgt tgataaataat gggaaaattc actatgcagg caaaaatatt
2820

gaagaaaaatg cgccagaatg gacactgaca cataaaaata atttggaaacc ttttactta
2880

acagttataa aaaaagccga taatcagacg ccactaaag gagcggaaatt ccgtttaca
2940

ggaccagata cgatattga attacaaaaa gatggcaaag aaacggatac ttttgggg
3000

aaaaacttaa aaccaggaa atatgttcta acagaaacct ttacgccc当地 aggatatcag
3060

gggttaaaag aaccaatcgataaatt cgtgaagatg gttcagtcac gatagatgg
3120

aaaaaagtag cagatgtttt aatttctgaa gagaagaata atcaaattac ttttagacgtt
3180

acgaaccaag caaaggttcc tttacctgaa actggggca taggacgctt gtggttttac
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P07741US01_6-19-06_Sequence.txt

3240

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3300

gggagtgtg
3309

<210> 9
<211> 1103
<212> PRT
<213> Staphylococcus epidermidis

<400> 9

Met Ile Thr Asp Glu Asn Asp Lys Thr Asn Ile Asn Ile Glu Leu Asn
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Leu Leu Asn Gln Thr Glu Gln Pro Leu Gln Arg Glu Ile Gln Leu Lys
20 25 30

Asn Ala Gln Phe Met Asp Thr Ala Val Ile Glu Lys Asp Gly Tyr Ser
35 40 45

Tyr Gln Val Thr Asn Gly Thr Leu Tyr Leu Thr Leu Asp Ala Gln Val
50 55 60

Lys Lys Pro Val Gln Leu Ser Leu Ala Val Glu Gln Ser Ser Leu Gln
65 70 75 80

Thr Ala Gln Pro Pro Lys Leu Leu Tyr Glu Asn Asn Glu Tyr Asp Val
85 90 95

Ser Val Thr Ser Glu Lys Ile Thr Val Glu Asp Ser Ala Lys Glu Ser
100 105 110

Thr Glu Pro Glu Lys Ile Thr Val Pro Glu Asn Thr Lys Glu Thr Asn
115 120 125

Lys Asn Asp Ser Ala Pro Glu Lys Thr Glu Gln Pro Thr Ala Thr Glu
130 135 140

P07741US01_6-19-06_Sequence.txt

Glu Val Thr Asn Pro Phe Ala Glu Ala Arg Met Ala Pro Ala Thr Leu
145 150 155 160

Arg Ala Asn Leu Ala Leu Pro Leu Ile Ala Pro Gln Tyr Thr Thr Asp
165 170 175

Asn Ser Gly Thr Tyr Pro Thr Ala Asn Trp Gln Pro Thr Gly Asn Gln
180 185 190

Asn Val Leu Asn His Gln Gly Asn Lys Asp Gly Ser Ala Gln Trp Asp
195 200 205

Gly Gln Thr Ser Trp Asn Gly Asp Pro Thr Asn Arg Thr Asn Ser Tyr
210 215 220

Ile Glu Tyr Gly Gly Thr Gly Asp Gln Ala Asp Tyr Ala Ile Arg Lys
225 230 235 240

Tyr Ala Arg Glu Thr Thr Pro Gly Leu Phe Asp Val Tyr Leu Asn
245 250 255

Val Arg Gly Asn Val Gln Lys Glu Ile Thr Pro Leu Asp Leu Val Leu
260 265 270

Val Val Asp Trp Ser Gly Ser Met Asn Glu Asn Asn Arg Ile Gly Glu
275 280 285

Val Gln Lys Gly Val Asn Arg Phe Val Asp Thr Leu Ala Asp Ser Gly
290 295 300

Ile Thr Asn Asn Ile Asn Met Gly Tyr Val Gly Tyr Ser Ser Asp Gly
305 310 315 320

Tyr Asn Asn Asn Ala Ile Gln Met Gly Pro Phe Asp Thr Val Lys Asn
325 330 335

Pro Ile Lys Asn Ile Thr Pro Ser Ser Thr Arg Gly Gly Thr Phe Thr
340 345 350

P07741US01_6-19-06_Sequence.txt

Gln Lys Ala Leu Arg Asp Ala Gly Asp Met Leu Ala Thr Pro Asn Gly
355 360 365

His Lys Lys Val Ile Val Leu Leu Thr Asp Gly Val Pro Thr Phe Ser
370 375 380

Tyr Lys Val Ser Arg Val Gln Thr Glu Ala Asp Gly Arg Phe Tyr Gly
385 390 395 400

Thr Gln Phe Thr Asn Arg Gln Asp Gln Pro Gly Ser Thr Ser Tyr Ile
405 410 415

Ser Gly Ser Tyr Asn Ala Pro Asp Gln Asn Asn Ile Asn Lys Arg Ile
420 425 430

Asn Ser Thr Phe Ile Ala Thr Ile Gly Glu Ala Met Val Leu Lys Gln
435 440 445

Arg Gly Ile Glu Ile His Gly Leu Gly Ile Gln Leu Gln Ser Asp Pro
450 455 460

Arg Ala Asn Leu Ser Lys Gln Gln Val Glu Asp Lys Met Arg Glu Met
465 470 475 480

Val Ser Ala Asp Glu Asn Gly Asp Leu Tyr Tyr Glu Ser Ala Asp Tyr
485 490 495

Ala Pro Asp Ile Ser Asp Tyr Leu Ala Lys Lys Ala Val Gln Ile Ser
500 505 510

Gly Thr Val Val Asn Gly Lys Val Val Asp Pro Ile Ala Glu Pro Phe
515 520 525

Lys Tyr Glu Pro Asn Thr Leu Ser Met Lys Ser Val Gly Pro Val Gln
530 535 540

Val Gln Thr Leu Pro Glu Val Ser Leu Thr Gly Ala Thr Ile Asn Ser
545 550 555 560

P07741US01_6-19-06_Sequence.txt

Asn Glu Ile Tyr Leu Gly Lys Gly Gln Glu Ile Gln Ile His Tyr Gln
565 570 575

Val Arg Ile Gln Thr Glu Ser Glu Asn Phe Lys Pro Asp Phe Trp Tyr
580 585 590

Gln Met Asn Gly Arg Thr Thr Phe Gln Pro Leu Ala Thr Ala Pro Glu
595 600 605

Lys Val Asp Phe Gly Val Pro Ser Gly Lys Ala Pro Gly Val Lys Leu
610 615 620

Asn Val Lys Lys Ile Trp Glu Glu Tyr Asp Gln Asp Pro Thr Ser Arg
625 630 635 640

Pro Asp Asn Val Ile Tyr Glu Ile Ser Arg Lys Gln Val Thr Asp Thr
645 650 655

Ala Asn Trp Gln Thr Gly Tyr Ile Lys Leu Ser Lys Pro Glu Asn Asp
660 665 670

Thr Ser Asn Ser Trp Glu Arg Lys Asn Val Thr Gln Leu Ser Lys Thr
675 680 685

Ala Asp Glu Ser Tyr Gln Glu Val Leu Gly Leu Pro Gln Tyr Asn Asn
690 695 700

Gln Gly Gln Ala Phe Asn Tyr Gln Thr Thr Arg Glu Leu Ala Val Pro
705 710 715 720

Gly Tyr Ser Gln Glu Lys Ile Asp Asp Thr Thr Trp Lys Asn Thr Lys
725 730 735

Gln Phe Lys Pro Leu Asp Leu Lys Val Ile Lys Asn Ser Ser Ser Gly
740 745 750

Glu Lys Asn Leu Val Gly Ala Val Phe Glu Leu Ser Gly Lys Asn Val
755 760 765

P07741US01_6-19-06_Sequence.txt

Gln Thr Thr Leu Val Asp Asn Lys Asp Gly Ser Tyr Ser Leu Pro Lys
770 775 780

Asp Val Arg Leu Gln Lys Gly Glu Arg Tyr Thr Leu Thr Glu Val Lys
785 790 795 800

Ala Pro Ala Gly His Glu Leu Gly Lys Lys Thr Thr Trp Gln Ile Glu
805 810 815

Val Ser Glu Gln Gly Lys Val Ser Ile Asp Gly Gln Glu Val Thr Thr
820 825 830

Thr Asn Gln Val Ile Pro Leu Glu Ile Glu Asn Lys Phe Ser Ser Leu
835 840 845

Pro Ile Arg Ile Arg Lys Tyr Thr Met Gln Asn Gly Lys Gln Val Asn
850 855 860

Leu Ala Glu Ala Thr Phe Ala Leu Gln Arg Lys Asn Ala Gln Gly Ser
865 870 875 880

Tyr Gln Thr Val Ala Thr Gln Lys Thr Asp Thr Thr Gly Leu Ser Tyr
885 890 895

Phe Lys Ile Ser Glu Pro Gly Glu Tyr Arg Met Val Glu Gln Ser Gly
900 905 910

Pro Leu Gly Tyr Asp Thr Leu Ala Gly Asn Tyr Glu Phe Thr Val Asp
915 920 925

Lys Tyr Gly Lys Ile His Tyr Ala Gly Lys Asn Ile Glu Glu Asn Ala
930 935 940

Pro Glu Trp Thr Leu Thr His Gln Asn Asn Leu Lys Pro Phe Asp Leu
945 950 955 960

Thr Val Asn Lys Lys Ala Asp Asn Gln Thr Pro Leu Lys Gly Ala Lys
965 970 975

P07741US01_6-19-06_Sequence.txt

Phe Arg Leu Thr Gly Pro Asp Thr Asp Ile Glu Leu Pro Lys Asp Gly
980 985 990

Lys Glu Thr Asp Thr Phe Val Phe Glu Asn Leu Lys Pro Gly Lys Tyr
995 1000 1005

Val Leu Thr Glu Thr Phe Thr Pro Glu Gly Tyr Gln Gly Leu Lys
1010 1015 1020

Glu Pro Ile Glu Leu Ile Ile Arg Glu Asp Gly Ser Val Thr Ile
1025 1030 1035

Asp Gly Glu Lys Val Ala Asp Val Leu Ile Ser Gly Glu Lys Asn
1040 1045 1050

Asn Gln Ile Thr Leu Asp Val Thr Asn Gln Ala Lys Val Pro Leu
1055 1060 1065

Pro Glu Thr Gly Ile Gly Arg Leu Trp Phe Tyr Leu Ile Ala
1070 1075 1080

Ile Ser Thr Phe Val Ile Ala Gly Val Tyr Leu Phe Ile Arg Arg
1085 1090 1095

Pro Glu Gly Ser Val
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<210> 10
<211> 1428
<212> DNA
<213> Staphylococcus epidermidis

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120

ttccctgtatg gtcaattacc agaacagcag caaaacacag gggaaagaggg aacgctgctt
180

caaaattatc ggggcttaaa tgacgtcact tatcaagtct atgatgtgac ggatccgttt
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P07741US01_6-19-06_Sequence.txt

240

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300

ggtgcaacaa atagaaaacc gatcgagaa gataaaacac agacaataaa tggagaagat
360

ggagtggttt cttttcatt agctagcaa gattcgcagc aacgagataa agcctattta
420

tttgttgaag cggaagcacc agaagtggta aaggaaaaag ctagcaacct agtagtgatt
480

ttgcctgttc aagatccaca agggcaatcg ttaacgcata ttcatttata tccaaaaaat
540

gaagaaaatg cctatgactt accaccactt gaaaaaacgg tactcgataa gcaacaaggc
600

ttaatcaag gagagcacat taactatcg ttaacgactc agattccagc gaatattttta
660

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720

tcaattgagg taaaagtggc tggaaaaaca gttactacag gttacacact gacgacgcaa
780

aagcatggat ttacgcttga ttttcaatt aaagacttac aaaactttgc aaatcaaaca
840

atgactgtgt cgtatcaa at gcgttagaa aagaccgctg aacctgacac tgcgattaac
900

aacgaaggac aattagtcac ggacaaacat accttgacta aaagagccac agttcgtaca
960

ggcggcaagt ctgttgc aaatgtatgt gaaaatgcga aaatcacctt gccagaggt
1020

gttttatcg tcaaaaatca agcggggaa tacctcaatg aaacagcaa cggtatcgt
1080

tggaaaaag aaaaagcatt agctaaaaaa ttcacgtcta atcaagccgg tgaattttca
1140

gttaaaggct taaaagatgg ccagtacttc ttgaaagaaa tctctgcacc aaaaggttat
1200

cttctgaatc aaacagaaat tcctttacg gtggaaaaa attcttatgc aacgaacgga
1260

P07741US01_6-19-06_Sequence.txt

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1320

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1380

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1428

<210> 11

<211> 476

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 11

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20 25 30

Gln Val Thr Leu His Lys Leu Leu Phe Pro Asp Gly Gln Leu Pro Glu
35 40 45

Gln Gln Gln Asn Thr Gly Glu Glu Gly Thr Leu Leu Gln Asn Tyr Arg
50 55 60

Gly Leu Asn Asp Val Thr Tyr Gln Val Tyr Asp Val Thr Asp Pro Phe
65 70 75 80

Tyr Gln Leu Arg Ser Glu Gly Lys Thr Val Gln Glu Ala Gln Arg Gln
85 90 95

Leu Ala Glu Thr Gly Ala Thr Asn Arg Lys Pro Ile Ala Glu Asp Lys
100 105 110

Thr Gln Thr Ile Asn Gly Glu Asp Gly Val Val Ser Phe Ser Leu Ala
115 120 125

Ser Lys Asp Ser Gln Gln Arg Asp Lys Ala Tyr Leu Phe Val Glu Ala
130 135 140

P07741US01_6-19-06_Sequence.txt

Glu Ala Pro Glu Val Val Lys Glu Lys Ala Ser Asn Leu Val Val Ile
145 150 155 160

Leu Pro Val Gln Asp Pro Gln Gly Gln Ser Leu Thr His Ile His Leu
165 170 175

Tyr Pro Lys Asn Glu Glu Asn Ala Tyr Asp Leu Pro Pro Leu Glu Lys
180 185 190

Thr Val Leu Asp Lys Gln Gln Gly Phe Asn Gln Gly Glu His Ile Asn
195 200 205

Tyr Gln Leu Thr Thr Gln Ile Pro Ala Asn Ile Leu Gly Tyr Gln Glu
210 215 220

Phe Arg Leu Ser Asp Lys Ala Asp Thr Thr Leu Thr Leu Leu Pro Glu
225 230 235 240

Ser Ile Glu Val Lys Val Ala Gly Lys Thr Val Thr Thr Gly Tyr Thr
245 250 255

Leu Thr Thr Gln Lys His Gly Phe Thr Leu Asp Phe Ser Ile Lys Asp
260 265 270

Leu Gln Asn Phe Ala Asn Gln Thr Met Thr Val Ser Tyr Gln Met Arg
275 280 285

Leu Glu Lys Thr Ala Glu Pro Asp Thr Ala Ile Asn Asn Glu Gly Gln
290 295 300

Leu Val Thr Asp Lys His Thr Leu Thr Lys Arg Ala Thr Val Arg Thr
305 310 315 320

Gly Gly Lys Ser Phe Val Lys Val Asp Ser Glu Asn Ala Lys Ile Thr
325 330 335

Leu Pro Glu Ala Val Phe Ile Val Lys Asn Gln Ala Gly Glu Tyr Leu
340 345 350

P07741US01_6-19-06_Sequence.txt

Asn Glu Thr Ala Asn Gly Tyr Arg Trp Gln Lys Glu Lys Ala Leu Ala
355 360 365

Lys Lys Phe Thr Ser Asn Gln Ala Gly Glu Phe Ser Val Lys Gly Leu
370 375 380

Lys Asp Gly Gln Tyr Phe Leu Glu Glu Ile Ser Ala Pro Lys Gly Tyr
385 390 395 400

Leu Leu Asn Gln Thr Glu Ile Pro Phe Thr Val Gly Lys Asn Ser Tyr
405 410 415

Ala Thr Asn Gly Gln Arg Thr Ala Pro Leu His Val Ile Asn Lys Lys
420 425 430

Val Lys Glu Ser Gly Phe Leu Pro Lys Thr Asn Glu Glu Arg Ser Ile
435 440 445

Trp Leu Thr Ile Ala Gly Leu Leu Ile Ile Gly Met Val Val Ile Trp
450 455 460

Leu Phe Tyr Gln Lys Gln Lys Arg Gly Glu Arg Lys
465 470 475

<210> 12
<211> 1881
<212> DNA
<213> Staphylococcus epidermidis

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120

ctcggttaccc acaaaaagaa aatgacggat ttaccagatc cgcttattca aaatagcggg
180

aaagaaaatga gcgagtttga taaatatcaa ggactggcag atgtgacgtt tagtatttt
240

P07741US01_6-19-06_Sequence.txt

aacgtgacga acgaatttta cgagcaacga gcggcaggcg caagcgttga tgcagctaaa
300
caagctgtcc aaagttaac tcctggaaa cctgttgctc aaggaaccac cgatgcaa
360
ggaatgtca ctgttcagtt acctaaaaaa caaatggta aagatgcagt gtataccatt
420
aaagaagaac caaaagaggg tgttagtgct gctacgaata tggtggtggc gttcccagtt
480
tacgaaatga tcaagcaaac agatggttcc tataaatatg gaacagaaga attagcggtt
540
gttcatattt atcctaaaaa tgtggtagcc aatgatggta gtttacatgt gaaaaaaagta
600
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660
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720
gataaagaac aagcaaaacg ctttattact gggaaaagtt atgaaattgg cgaaaatgat
780
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840
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900
acaccattta caattgaagc aaacaatcaa acacctgttggaaaacacagt caaaaatgat
960
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aaaattaaat atcaaatttc tgtaaatatt ccattggggta ttgcagacaa agaaggcgac
1080
gctaataat acgtcaaattt caatggatgataa acatg atgcagcctt aactttgtat
1140
aacgtgactt ctggagagta tgcttatgcg ttatatgttggataacagt gattgctc
1200
gaaaattatc aagtgactga acaagcaaat ggcttcactg tcgccccaa tccagcgtat
1260
attcctacgc taacaccagg cgccacacta aaattcggttt actttatgca tttaaatgaa

P07741US01_6-19-06_Sequence.txt

1320

aaagcagatc ctacgaaagg ctttaaaaat gaggcgaatg ttgataacgg tcataccgac
1380

gaccaaacac caccaactgt tgaagttgt acaggtggga aacgttcat taaagtcgt
1440

ggcgatgtga cagcgacaca agccttggcg ggagcttcct ttgtcgtccg tgatcaaaac
1500

agcgacacag caaatttattt gaaaatcgat gaaacaacga aagcagcaac ttgggtgaaa
1560

acaaaaagctg aagcaactac ttttacaaca acggctgatg gattagttga tatcacaggg
1620

cttaaatacg gtaccttatta tttagaagaa actgttagctc ctgatgatta tgtcttgtta
1680

acaatcgga ttgaatttgt ggtcaatgaa caatcatatg gcacaacaga aaacctagt
1740

tcaccagaaa aagtaccaaa caaacacaaa ggtaccttac cttcaacagg tggcaaagga
1800

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1860

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1881

<210> 13

<211> 627

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 13

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1 5 10 15

Ile Leu Pro Leu Phe Thr Ser Val Leu Gly Thr Thr Ala Phe Ala
20 25 30

Glu Glu Asn Gly Glu Ser Ala Gln Leu Val Ile His Lys Lys Lys Met
35 40 45

P07741US01_6-19-06_Sequence.txt

Thr Asp Leu Pro Asp Pro Leu Ile Gln Asn Ser Gly Lys Glu Met Ser
50 55 60

Glu Phe Asp Lys Tyr Gln Gly Leu Ala Asp Val Thr Phe Ser Ile Tyr
65 70 75 80

Asn Val Thr Asn Glu Phe Tyr Glu Gln Arg Ala Ala Gly Ala Ser Val
85 90 95

Asp Ala Ala Lys Gln Ala Val Gln Ser Leu Thr Pro Gly Lys Pro Val
100 105 110

Ala Gln Gly Thr Thr Asp Ala Asn Gly Asn val Thr val Gln Leu Pro
115 120 125

Lys Lys Gln Asn Gly Lys Asp Ala Val Tyr Thr Ile Lys Glu Glu Pro
130 135 140

Lys Glu Gly val val Ala Ala Thr Asn Met val val Ala Phe Pro Val
145 150 155 160

Tyr Glu Met Ile Lys Gln Thr Asp Gly Ser Tyr Lys Tyr Gly Thr Glu
165 170 175

Glu Leu Ala Val Val His Ile Tyr Pro Lys Asn Val Val Ala Asn Asp
180 185 190

Gly Ser Leu His Val Lys Lys Val Gly Thr Ala Glu Asn Glu Gly Leu
195 200 205

Asn Gly Ala Glu Phe Val Ile Ser Lys Ser Glu Gly Ser Pro Gly Thr
210 215 220

Val Lys Tyr Ile Gln Gly Val Lys Asp Gly Leu Tyr Thr Trp Thr Thr
225 230 235 240

Asp Lys Glu Gln Ala Lys Arg Phe Ile Thr Gly Lys Ser Tyr Glu Ile
245 250 255

P07741US01_6-19-06_Sequence.txt

Gly Glu Asn Asp Phe Thr Glu Ala Glu Asn Gly Thr Gly Glu Leu Thr
260 265 270

Val Lys Asn Leu Glu Val Gly Ser Tyr Ile Leu Glu Glu Val Lys Ala
275 280 285

Pro Asn Asn Ala Glu Leu Ile Glu Asn Gln Thr Lys Thr Pro Phe Thr
290 295 300

Ile Glu Ala Asn Asn Gln Thr Pro Val Glu Lys Thr Val Lys Asn Asp
305 310 315 320

Thr Ser Lys Val Asp Lys Thr Thr Pro Ser Leu Asp Gly Lys Asp Val
325 330 335

Ala Ile Gly Glu Lys Ile Lys Tyr Gln Ile Ser Val Asn Ile Pro Leu
340 345 350

Gly Ile Ala Asp Lys Glu Gly Asp Ala Asn Lys Tyr Val Lys Phe Asn
355 360 365

Leu Val Asp Lys His Asp Ala Ala Leu Thr Phe Asp Asn Val Thr Ser
370 375 380

Gly Glu Tyr Ala Tyr Ala Leu Tyr Asp Gly Asp Thr Val Ile Ala Pro
385 390 395 400

Glu Asn Tyr Gln Val Thr Glu Gln Ala Asn Gly Phe Thr Val Ala Val
405 410 415

Asn Pro Ala Tyr Ile Pro Thr Leu Thr Pro Gly Gly Thr Leu Lys Phe
420 425 430

Val Tyr Phe Met His Leu Asn Glu Lys Ala Asp Pro Thr Lys Gly Phe
435 440 445

Lys Asn Glu Ala Asn Val Asp Asn Gly His Thr Asp Asp Gln Thr Pro
450 455 460

P07741US01_6-19-06_Sequence.txt

Pro Thr Val Glu Val Val Thr Gly Gly Lys Arg Phe Ile Lys Val Asp
465 470 475 480

Gly Asp Val Thr Ala Thr Gln Ala Leu Ala Gly Ala Ser Phe Val Val
485 490 495

Arg Asp Gln Asn Ser Asp Thr Ala Asn Tyr Leu Lys Ile Asp Glu Thr
500 505 510

Thr Lys Ala Ala Thr Trp Val Lys Thr Lys Ala Glu Ala Thr Thr Phe
515 520 525

Thr Thr Thr Ala Asp Gly Leu Val Asp Ile Thr Gly Leu Lys Tyr Gly
530 535 540

Thr Tyr Tyr Leu Glu Glu Thr Val Ala Pro Asp Asp Tyr Val Leu Leu
545 550 555 560

Thr Asn Arg Ile Glu Phe Val Val Asn Glu Gln Ser Tyr Gly Thr Thr
565 570 575

Glu Asn Leu Val Ser Pro Glu Lys Val Pro Asn Lys His Lys Gly Thr
580 585 590

Leu Pro Ser Thr Gly Gly Lys Gly Ile Tyr Val Tyr Leu Gly Ser Gly
595 600 605

Ala Val Leu Leu Leu Ile Ala Gly Val Tyr Phe Ala Arg Arg Arg Lys
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Glu Asn Ala
625

<210> 14
<211> 3387
<212> DNA
<213> Staphylococcus epidermidis

<400> 14
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P07741US01_6-19-06_Sequence.txt

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120
atttcagctg aagtcatatc ggatcagtct gaaaaaaaag cactgaacat caagctaaat
180
gcgaataaca ccagtgctga aaagatagaa aaagaaattt gttctagtcga aaattactta
240
agtgtatgtgg aaagaaaaga aggagatggc tatgcttatac aggtaaatag cggaaaatt
300
acgttggaaa tctcatcaaa cactaaacaa actatcgatc tgagtttcc aatcgatcca
360
gcactttacc acagccaggc aaacaagctg atcgtcgata ataaagaata tgacattatt
420
gatgagacag aaaataagaa agatacagat gtgtcagtac caaagccaga cgaaatagaa
480
gaagaatcat caaaagaaaa cggaaaattct gtcagccat ttacattgcc tacattatcc
540
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cagggcactt atcctaaagc cagttggcaa cctacaggaa atacaatgt tcctgatcat
660
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720
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780
atacgaaagt atgcaaagga aacaagtaca cccggattgt ttgatgtta tttgaatgct
840
cgtggaaatg tacaaaaaga tatcacgcct cttgatctcg tattggtcgt agactggtca
900
ggaagtatga acgacaataa tcggatcggt gaagtaaaga ttgggtgcga tcgtttgtc
960
gatactttag cagatagcgg tatcacagac aaaatcaata tggatgtt cggctactca
1020
agcgaaggat atagctacag taacggtgca gtacagatgg gttcatttga ttcagtgaaa
1080

P07741US01_6-19-06_Sequence.txt

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1200

ctgacggatg gtgtaccaac atttcctat aaagtacagc ggtacacgc acaatcaagc
1260

agcaattatt acggaactca gtttctaatt acgcaagatc ggccggaaa tacttctcta
1320

atctcaagaa tctatgatgc acctgaccaa aacaatctat ccagaagaat cgacagtacg
1380

tttatcgcaa ccatcgaga agcgatggca ctcaaagaac gaggaatcga aatacatggt
1440

cttggcatcc aacttcaaag cgatccggca gctggtctct caaaaggcaga agtagagtct
1500

cgtatgcgac aaatggtttc atcagatgaa aaaggcgatc tttactatga atcagctgat
1560

catgcaacag atatctctga atacctagcc aaaaaagctg tacagatctc agcaactgta
1620

agcaatggac aaataaatga tccaatcgca gaaccattca tttatcagcc tggcacactt
1680

tcagtcaaga gtgtgggac aagtcctaca acggtcactc catctatttc catagaagga
1740

aataccatca agagcaatca gatctattta ggaaaagacc aagaaatcca aatccattac
1800

caagtgagaa tccaaacaga aatgaggac ttccatccaa atttctggta tcaaataaac
1860

ggcaggacaa cttccagcc aaacattgat accaatgaat tagctgaatt cggatacc
1920

tctgctaaag ctccggagt cagtcttcac ataaaaaagt tatggaaaga atttgacaac
1980

aatctagctg atcgccaga tcaagttact tttgagattc aacggaaaca tacgacaaat
2040

gctgcagctt ggaaaaacgg atatattcga atcattaaac cagctaaaga tacaacaaat
2100

acgtggaaac gtgcagacat tgacaaatta tctgcaaata gcggagaaag ttatcaagag
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P07741US01_6-19-06_Sequence.txt

2160

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2220

gaattacctg taccaggata cgattctcaa caaatagatg caatgacatg gaaaaatact
2280

aaacaattca caccgttaaa cttgaaaata acgaaaaatt cctctacagg tggaaaaggat
2340

cttattggcg ctgtttcaa attaacagga gattctattg atactttact aacagatcat
2400

ggcgacggaa cctattctct tccagaaaaat gtcaaattgc aaaaagaaat gacctatacg
2460

ctgacagaaaa caaaagctcc agaaggcat ggattaagca aaaagactac ttgggaaatc
2520

aagatcgctt ctgatggtagt ggttaaccatt gatggaaaaa cagtcactac ttccgatgat
2580

acgatccagt tgactattga aaatcctttt gttgaagttc ctgttagcagt acgttgtat
2640

gcgatgcaag ggacggacaa agagataaat cttaaaggag cagcatttc cctacagaaa
2700

aaagaagcaa atggtaactta tcagccaatt gacagccaaa caacgaatga aaaaggctt
2760

gccagtttg attcactcac acctggtaaa tatcgagtgc ttgaaacagc tggcctgcc
2820

ggatatgata cttcgccggg aaattatgaa ttccaaatcg ataaatatgg aaaaatcatt
2880

tacacggaa aaaataccga gatgacaaat aatgtatgga cgctcactca tcaaaatcga
2940

ctaaaagcgt ttgatctaac ggtacacaaa aaagaagaca acggacagac attaaaagga
3000

gcaaaattca gactgcaggg accagaaatg gacttagaat cgccaaaaga tggacaagaa
3060

acagataacct ttctattcga aaatttaaaa cctggaactt atacgctgac cgtttttt
3120

acaccagaag gataccaagg tctaaaagag ccagttacta tagttataca cgaagatggg
3180

P07741US01_6-19-06_Sequence.txt

tcaattcaag tggatggaca agatcatgaa tctgttctgt caccaggagc caaaaacaac
3240

cagatttctt tagacatcac gaatcaggca aaagtaccat tacctgaaac gggaggaatt
3300

ggccgttttag gaatctatct agtagggatg attggttgtg cgttttctat ttggtatctt
3360

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3387

<210> 15

<211> 1129

<212> PRT

<213> Staphylococcus epidermidis

<400> 15

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20 25 30

Asp Asp Pro Thr Val Leu Glu Thr Ile Ser Ala Glu Val Ile Ser Asp
35 40 45

Gln Ser Gly Lys Lys Ala Leu Asn Ile Lys Leu Asn Ala Asn Asn Thr
50 55 60

Ser Ala Glu Lys Ile Glu Lys Glu Ile Gly Leu Val Glu Asn Tyr Leu
65 70 75 80

Ser Asp Val Glu Arg Lys Glu Gly Asp Gly Tyr Ala Tyr Gln Val Asn
85 90 95

Ser Gly Lys Ile Thr Leu Glu Ile Ser Ser Asn Thr Lys Gln Thr Ile
100 105 110

Asp Leu Ser Phe Pro Ile Asp Pro Ala Leu Tyr His Ser Gln Ala Asn
115 120 125

P07741US01_6-19-06_Sequence.txt

Lys Leu Ile Val Asp Asn Lys Glu Tyr Asp Ile Ile Asp Glu Thr Glu
130 135 140

Asn Lys Lys Asp Thr Asp Val Ser Val Pro Lys Pro Asp Glu Ile Glu
145 150 155 160

Glu Glu Ser Ser Lys Glu Asn Glu Asn Ser Val Ser Pro Phe Thr Leu
165 170 175

Pro Thr Leu Ser Leu Pro Ala Val Ser Val Pro Ser Asn Gln Thr Ile
180 185 190

Pro Thr Glu Tyr Thr Thr Asp Asp Gln Gly Thr Tyr Pro Lys Ala Ser
195 200 205

Trp Gln Pro Thr Gly Asn Thr Asn Val Leu Asp His Gln Gly Asn Lys
210 215 220

Asn Gly Thr Asn Gln Trp Asp Gly Ile Asn Ser Trp Asn Gly Asp Pro
225 230 235 240

Asn Asp Arg Thr His Ser Tyr Ile Glu Tyr Gly Gly Thr Gly Asn Gln
245 250 255

Ala Asp Tyr Ala Ile Arg Lys Tyr Ala Lys Glu Thr Ser Thr Pro Gly
260 265 270

Leu Phe Asp Val Tyr Leu Asn Ala Arg Gly Asn Val Gln Lys Asp Ile
275 280 285

Thr Pro Leu Asp Leu Val Leu Val Val Asp Trp Ser Gly Ser Met Asn
290 295 300

Asp Asn Asn Arg Ile Gly Glu Val Lys Ile Gly Val Asp Arg Phe Val
305 310 315 320

Asp Thr Leu Ala Asp Ser Gly Ile Thr Asp Lys Ile Asn Met Gly Tyr
325 330 335

P07741US01_6-19-06_Sequence.txt

Val Gly Tyr Ser Ser Glu Gly Tyr Ser Tyr Ser Asn Gly Ala Val Gln
340 345 350

Met Gly Ser Phe Asp Ser Val Lys Asn Gln Val Lys Ser Ile Thr Pro
355 360 365

Ser Arg Thr Asn Gly Gly Thr Phe Thr Gln Lys Ala Leu Arg Asp Ala
370 375 380

Gly Ser Met Leu Ser Val Pro Asn Gly His Lys Lys Val Ile Val Leu
385 390 395 400

Leu Thr Asp Gly Val Pro Thr Phe Ser Tyr Lys Val Gln Arg Val His
405 410 415

Ala Gln Ser Ser Asn Tyr Tyr Gly Thr Gln Phe Ser Asn Thr Gln
420 425 430

Asp Arg Pro Gly Asn Thr Ser Leu Ile Ser Arg Ile Tyr Asp Ala Pro
435 440 445

Asp Gln Asn Asn Leu Ser Arg Arg Ile Asp Ser Thr Phe Ile Ala Thr
450 455 460

Ile Gly Glu Ala Met Ala Leu Lys Glu Arg Gly Ile Glu Ile His Gly
465 470 475 480

Leu Gly Ile Gln Leu Gln Ser Asp Pro Ala Ala Gly Leu Ser Lys Ala
485 490 495

Glu Val Glu Ser Arg Met Arg Gln Met Val Ser Ser Asp Glu Lys Gly
500 505 510

Asp Leu Tyr Tyr Glu Ser Ala Asp His Ala Thr Asp Ile Ser Glu Tyr
515 520 525

Leu Ala Lys Lys Ala Val Gln Ile Ser Ala Thr Val Ser Asn Gly Gln
530 535 540

P07741US01_6-19-06_Sequence.txt

Ile Asn Asp Pro Ile Ala Glu Pro Phe Ile Tyr Gln Pro Gly Thr Leu
545 550 555 560

Ser Val Lys Ser Val Gly Thr Ser Pro Thr Thr Val Thr Pro Ser Ile
565 570 575

Ser Ile Glu Gly Asn Thr Ile Lys Ser Asn Gln Ile Tyr Leu Gly Lys
580 585 590

Asp Gln Glu Ile Gln Ile His Tyr Gln Val Arg Ile Gln Thr Glu Asn
595 600 605

Glu Asp Phe His Pro Asn Phe Trp Tyr Gln Met Asn Gly Arg Thr Thr
610 615 620

Phe Gln Pro Asn Ile Asp Thr Asn Glu Leu Ala Glu Phe Gly Ile Pro
625 630 635 640

Ser Ala Lys Ala Pro Gly Val Ser Leu His Ile Lys Lys Leu Trp Glu
645 650 655

Glu Phe Asp Asn Asn Leu Ala Asp Arg Pro Asp Gln Val Thr Phe Glu
660 665 670

Ile Gln Arg Glu His Thr Thr Asn Ala Ala Ala Trp Lys Asn Gly Tyr
675 680 685

Ile Arg Ile Ile Lys Pro Ala Lys Asp Thr Thr Asn Thr Trp Glu Arg
690 695 700

Ala Asp Ile Asp Lys Leu Ser Ala Asn Ser Gly Glu Ser Tyr Gln Glu
705 710 715 720

Ile Leu Ser Leu Pro Gln Tyr Asn Asn Gln Gly Gln Ala Phe Ser Tyr
725 730 735

Gln Thr Ile Lys Glu Leu Pro Val Pro Gly Tyr Asp Ser Gln Gln Ile
740 745 750

P07741US01_6-19-06_Sequence.txt

Asp Ala Met Thr Trp Lys Asn Thr Lys Gln Phe Thr Pro Leu Asn Leu
755 760 765

Lys Ile Thr Lys Asn Ser Ser Thr Gly Glu Lys Asp Leu Ile Gly Ala
770 775 780

Val Phe Lys Leu Thr Gly Asp Ser Ile Asp Thr Leu Leu Thr Asp His
785 790 795 800

Gly Asp Gly Thr Tyr Ser Leu Pro Glu Asn Val Lys Leu Gln Lys Glu
805 810 815

Met Thr Tyr Thr Leu Thr Glu Thr Lys Ala Pro Glu Gly His Gly Leu
820 825 830

Ser Lys Lys Thr Thr Trp Glu Ile Lys Ile Ala Ser Asp Gly Thr Val
835 840 845

Thr Ile Asp Gly Lys Thr Val Thr Thr Ser Asp Asp Thr Ile Gln Leu
850 855 860

Thr Ile Glu Asn Pro Phe Val Glu Val Pro Val Ala Val Arg Lys Tyr
865 870 875 880

Ala Met Gln Gly Thr Asp Lys Glu Ile Asn Leu Lys Gly Ala Ala Phe
885 890 895

Ser Leu Gln Lys Lys Glu Ala Asn Gly Thr Tyr Gln Pro Ile Asp Ser
900 905 910

Gln Thr Thr Asn Glu Lys Gly Leu Ala Ser Phe Asp Ser Leu Thr Pro
915 920 925

Gly Lys Tyr Arg Val Val Glu Thr Ala Gly Pro Ala Gly Tyr Asp Thr
930 935 940

Ser Pro Gly Asn Tyr Glu Phe Gln Ile Asp Lys Tyr Gly Lys Ile Ile
945 950 955 960

P07741US01_6-19-06_Sequence.txt

Tyr Thr Gly Lys Asn Thr Glu Met Thr Asn Asn Val Trp Thr Leu Thr
965 970 975

His Gln Asn Arg Leu Lys Ala Phe Asp Leu Thr Val His Lys Lys Glu
980 985 990

Asp Asn Gly Gln Thr Leu Lys Gly Ala Lys Phe Arg Leu Gln Gly Pro
995 1000 1005

Glu Met Asp Leu Glu Ser Pro Lys Asp Gly Gln Glu Thr Asp Thr
1010 1015 1020

Phe Leu Phe Glu Asn Leu Lys Pro Gly Thr Tyr Thr Leu Thr Glu
1025 1030 1035

Thr Phe Thr Pro Glu Gly Tyr Gln Gly Leu Lys Glu Pro Val Thr
1040 1045 1050

Ile Val Ile His Glu Asp Gly Ser Ile Gln Val Asp Gly Gln Asp
1055 1060 1065

His Glu Ser Val Leu Ser Pro Gly Ala Lys Asn Asn Gln Ile Ser
1070 1075 1080

Leu Asp Ile Thr Asn Gln Ala Lys Val Pro Leu Pro Glu Thr Gly
1085 1090 1095

Gly Ile Gly Arg Leu Gly Ile Tyr Leu Val Gly Met Ile Gly Cys
1100 1105 1110

Ala Phe Ser Ile Trp Tyr Leu Phe Leu Lys Lys Glu Arg Gly Gly
1115 1120 1125

Ser

<210> 16
<211> 1422
<212> DNA

P07741US01_6-19-06_Sequence.txt

<213> *Staphylococcus epidermidis*

<400> 16

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120

ttcccaaacg ggcaactgcc gaaaaatcat ccaaattgacg gacaagaaaa agctttatta
180

caaacgtatc gaggattaaa tggtgtcaca ttccaagttt atgatgtcac agattcttt
240

taccatctac gggaaaaggg caaaacggta gaagaagcac aagcagagat cgcaaaaaac
300

ggtgctt ccgttatgtt taccgcagaa gcaacaacta caactcttaa caacgaagat
360

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420

ttcattgaat ccaaagtacc agaagtcgtc aaagaaaaagg cagagaatat ggtagttgtt
480

cttcctgtac atggacaaaaa caatcaaaaaa ctttcaacta tccatttcta tcctaaaaat
540

gaagaaaaacg actaccctga tccacccccc gagaaggtat tagaagagcc tagaaatgat
600

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660

gactatcaaa agttcgaatt gtcagatgt gcggatgaag cattaacgtt tttacctaatt
720

agtttaacga tttcatcgaa tggagaaaag ctgacagaag gctttgtcat acacaagaaa
780

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840

ctgaccattt cttatcagat gcagctaagc agtacagcac aggcaacaa gaaaaatcaac
900

aacaacggaa cactggattt tggtttttgtt gtcagtacaa agaaagtctc tgtatataca
960

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P07741US01_6-19-06_Sequence.txt

1020

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1080

tggacaaaga acgaatcaga tgcgcttcac ctgatttccg ataaaaatgg cgcttttca
1140

atttccgggt tgaaaacagg aagttatcga taaaaagaga tcgaagcacc ttctggttat
1200

attttaagtg aaacagaaaat tccgttacc atttcaactt ttctttctga ggataaagag
1260

gcggacagta tattgaaagt agtcaataaa aaagaaaata gccgtccatt tcttccaaaa
1320

acaaacgaaa cgaaaaatac acttttaggc gttgttgta tggtattcgc aagcttgca
1380

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1422

<210> 17

<211> 473

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 17

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Gln Ile Thr Leu His Lys Leu Leu Phe Pro Asn Gly Gln Leu Pro Lys
35 40 45

Asn His Pro Asn Asp Gly Gln Glu Lys Ala Leu Leu Gln Thr Tyr Arg
50 55 60

Gly Leu Asn Gly Val Thr Phe Gln Val Tyr Asp Val Thr Asp Ser Phe
65 70 75 80

Tyr His Leu Arg Glu Lys Gly Lys Thr Val Glu Glu Ala Gln Ala Glu
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P07741US01_6-19-06_Sequence.txt

85

90

95

Ile Ala Lys Asn Gly Ala Ser Ser Gly Met Phe Thr Ala Glu Ala Thr
 100 105 110

Thr Thr Thr Leu Asn Asn Glu Asp Gly Ile Ala Ser Phe Ser Leu Ala
 115 120 125

Ala Lys Asp Gln Glu Lys Arg Asp Lys Ala Tyr Leu Phe Ile Glu Ser
 130 135 140

Lys Val Pro Glu Val Val Lys Glu Lys Ala Glu Asn Met Val Val Val
 145 150 155 160

Leu Pro Val His Gly Gln Asn Asn Gln Lys Leu Ser Thr Ile His Leu
 165 170 175

Tyr Pro Lys Asn Glu Glu Asn Asp Tyr Pro Asp Pro Pro Phe Glu Lys
 180 185 190

Val Leu Glu Glu Pro Arg Asn Asp Phe Thr Ile Gly Glu Lys Ile Thr
 195 200 205

Tyr Ser Leu His Thr Thr Ile Pro Val Asn Ile Leu Asp Tyr Gln Lys
 210 215 220

Phe Glu Leu Ser Asp Ser Ala Asp Glu Ala Leu Thr Phe Leu Pro Asn
 225 230 235 240

Ser Leu Thr Ile Ser Ser Asn Gly Glu Lys Leu Thr Glu Gly Phe Val
 245 250 255

Ile His Lys Lys Pro His Gly Phe Asp Val Leu Phe Ser Ile Pro Ser
 260 265 270

Leu Glu Lys Tyr Ala Gly Lys Lys Leu Thr Ile Ser Tyr Gln Met Gln
 275 280 285

Leu Ser Ser Thr Ala Gln Ala Asn Lys Glu Ile Asn Asn Asn Gly Thr
 Page 57

P07741US01_6-19-06_Sequence.txt

290

295

300

Leu Asp Phe Gly Phe Gly Val Ser Thr Lys Lys Val Ser Val Tyr Thr
 305 310 315 320

Gly Ser Lys Gln Phe Val Lys Ile Glu Thr Asn Lys Pro Asp Lys Arg
 325 330 335

Leu Ala Gly Ala Val Phe Leu Ile Lys Asn Lys Ala Gly Asn Tyr Leu
 340 345 350

Gln Gln Thr Ala Asn Gly Tyr Lys Trp Thr Lys Asn Glu Ser Asp Ala
 355 360 365

Leu His Leu Ile Ser Asp Lys Asn Gly Ala Phe Ser Ile Ser Gly Leu
 370 375 380

Lys Thr Gly Ser Tyr Arg Leu Lys Glu Ile Glu Ala Pro Ser Gly Tyr
 385 390 395 400

Ile Leu Ser Glu Thr Glu Ile Pro Phe Thr Ile Ser Thr Phe Leu Ser
 405 410 415

Glu Asp Lys Glu Ala Asp Ser Ile Leu Lys Val Val Asn Lys Lys Glu
 420 425 430

Asn Ser Arg Pro Phe Leu Pro Lys Thr Asn Glu Thr Lys Asn Thr Leu
 435 440 445

Leu Gly Val Val Gly Met Val Phe Ala Ser Phe Ala Ile Trp Leu Phe
 450 455 460

Ile Lys Lys Arg Thr Gly Val Lys Lys
 465 470

<210> 18
<211> 1878
<212> DNA
<213> Staphylococcus epidermidis

P07741US01_6-19-06_Sequence.txt

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120

cttcataaaa agaaaatgac tgatttaccc gatccttaa tccaaaacag cggaaaga
180

atgagcgaat tcgatcaata ccaaggatta gccgatattt cattttcagt ttataacgtc
240

actcaagaat tttatgcgca acgagataaa ggagcgtccg tggatgcagc aaaacaaga
300

gtccagtctt tgactcctgg tacaccagtt gtttcaggaa cgacagatgc tcatggaaat
360

gtcactttat cttaacctaa aaaacaaaat gggaaagatg cagtctacac gatcaaaga
420

gaaccaaaag acggagtgtc agctgccgca aacatggtt tagttccc tgtatatgag
480

atgatcaaac aagcagatgg ctcttataaa tacggacag aagaactaga tactatccat
540

ctctacccta aaaatacagt cgtaatgtat ggaacgttga aagttacaaa aatcggtact
600

gccgaaaacg aagcactaaa tggagcagaa tttattttt ctaaagaaga aggaacacca
660

agcgtcaaaa aatacatcca aagtgtcaca gatggattgt acactggac aactgatcaa
720

accaaagcca aacatttcat tactggtcat tcttatgaca tcggcaacaa tgactttgcc
780

gaggcatcta ttgaaaaagg ccagttgatc gttaatcatt tagaagttgg aaaatataat
840

ttagaagaag taaaagctcc tgataatgcg gaaatgattt gaaagcaaac aatcacgcct
900

tttgagatcc tggcaaatacg ccaaacacca gtagaaaaga ccatcaaaaa tgatacgtct
960

aaagttgata aaacaacacc tcaattgaat gggaaagatg tcgcaatcg gttaaaaatt
1020

P07741US01_6-19-06_Sequence.txt

caaatatgaga tttctgtcaa tatcccatta ggtatcgctg ataaagaagg aacgc当地
1080
aagtacacaa cattcaaact tatcgatact catgacgctg cttaaacatt tgataatgat
1140
tcttcagggaa cgtatgctta tgccttatat gatggaaata aagaaatcga cccagtaat
1200
tattctgtca ctgagcaaac agacggattc acggtttag ttgatccaa ttatattcct
1260
tcattaactc ctggcgtac attgaaattc gtttactata tgcatttcaa cgaaaaagca
1320
gatccaacca aaggattttc taaccaagca aatgtcgata acgggcatac aaatgatcaa
1380
acaccaccgt cagtcgatgt cgttactggg ggcaaacgat ttgttaaagt agatggtgac
1440
gttacatcg accaaacact tgctggagca gaattcgtcg ttcgtgatca agatagtgac
1500
acagcgaaat atttatcgat cgaccatcc acaaaagccg tcagctgggt atcggcgaaa
1560
gaatcagcaa cggttttac aaccacaagt aacggttaa tcgatgtgac aggtctaaaa
1620
tatggcacgt actatctgga agaaacgaaa gcgccagaaa aatatgttcc attaacaac
1680
cgtgttagcat ttactatcgta tgaacaatct tatgtAACAG caggacagtt gatttctcct
1740
gaaaaaatac caaataaaaca caaaggtaa cttccttcaa caggcgtaa gggaaatctat
1800
gtgtatatcg gtgcaggagt agtccttcta ctgattgctg gactgtactt tgctagacgc
1860
aagcacagtc agatttag
1878

<210> 19
<211> 625
<212> PRT
<213> Staphylococcus epidermidis

<400> 19

P07741US01_6-19-06_Sequence.txt

Met Lys Asn His Lys Lys Ile Asn Val Met Leu Gly Val Leu Phe Leu
1 5 10 15

Ile Leu Pro Leu Leu Thr Asn Ser Phe Gly Ala Lys Lys Val Phe Ala
20 25 30

Glu Glu Thr Ala Ala Gln Val Ile Leu His Lys Lys Met Thr Asp
35 40 45

Leu Pro Asp Pro Leu Ile Gln Asn Ser Gly Lys Glu Met Ser Glu Phe
50 55 60

Asp Gln Tyr Gln Gly Leu Ala Asp Ile Ser Phe Ser Val Tyr Asn Val
65 70 75 80

Thr Gln Glu Phe Tyr Ala Gln Arg Asp Lys Gly Ala Ser Val Asp Ala
85 90 95

Ala Lys Gln Ala Val Gln Ser Leu Thr Pro Gly Thr Pro Val Ala Ser
100 105 110

Gly Thr Thr Asp Ala Asp Gly Asn Val Thr Leu Ser Leu Pro Lys Lys
115 120 125

Gln Asn Gly Lys Asp Ala Val Tyr Thr Ile Lys Glu Glu Pro Lys Asp
130 135 140

Gly Val Ser Ala Ala Ala Asn Met Val Leu Ala Phe Pro Val Tyr Glu
145 150 155 160

Met Ile Lys Gln Ala Asp Gly Ser Tyr Lys Tyr Gly Thr Glu Glu Leu
165 170 175

Asp Thr Ile His Leu Tyr Pro Lys Asn Thr Val Gly Asn Asp Gly Thr
180 185 190

Leu Lys Val Thr Lys Ile Gly Thr Ala Glu Asn Glu Ala Leu Asn Gly
195 200 205

P07741US01_6-19-06_Sequence.txt

Ala Glu Phe Ile Ile Ser Lys Glu Glu Gly Thr Pro Ser Val Lys Lys
210 215 220

Tyr Ile Gln Ser Val Thr Asp Gly Leu Tyr Thr Trp Thr Thr Asp Gln
225 230 235 240

Thr Lys Ala Lys His Phe Ile Thr Gly His Ser Tyr Asp Ile Gly Asn
245 250 255

Asn Asp Phe Ala Glu Ala Ser Ile Glu Lys Gly Gln Leu Ile Val Asn
260 265 270

His Leu Glu Val Gly Lys Tyr Asn Leu Glu Glu Val Lys Ala Pro Asp
275 280 285

Asn Ala Glu Met Ile Glu Lys Gln Thr Ile Thr Pro Phe Glu Ile Leu
290 295 300

Ala Asn Ser Gln Thr Pro Val Glu Lys Thr Ile Lys Asn Asp Thr Ser
305 310 315 320

Lys Val Asp Lys Thr Thr Pro Gln Leu Asn Gly Lys Asp Val Ala Ile
325 330 335

Gly Glu Lys Ile Gln Tyr Glu Ile Ser Val Asn Ile Pro Leu Gly Ile
340 345 350

Ala Asp Lys Glu Gly Thr Gln Asn Lys Tyr Thr Thr Phe Lys Leu Ile
355 360 365

Asp Thr His Asp Ala Ala Leu Thr Phe Asp Asn Asp Ser Ser Gly Thr
370 375 380

Tyr Ala Tyr Ala Leu Tyr Asp Gly Asn Lys Glu Ile Asp Pro Val Asn
385 390 395 400

Tyr Ser Val Thr Glu Gln Thr Asp Gly Phe Thr Val Ser Val Asp Pro
405 410 415

P07741US01_6-19-06_Sequence.txt

Asn Tyr Ile Pro Ser Leu Thr Pro Gly Gly Thr Leu Lys Phe Val Tyr
420 425 430

Tyr Met His Leu Asn Glu Lys Ala Asp Pro Thr Lys Gly Phe Ser Asn
435 440 445

Gln Ala Asn Val Asp Asn Gly His Thr Asn Asp Gln Thr Pro Pro Ser
450 455 460

Val Asp Val Val Thr Gly Gly Lys Arg Phe Val Lys Val Asp Gly Asp
465 470 475 480

Val Thr Ser Asp Gln Thr Leu Ala Gly Ala Glu Phe Val Val Arg Asp
485 490 495

Gln Asp Ser Asp Thr Ala Lys Tyr Leu Ser Ile Asp Pro Ser Thr Lys
500 505 510

Ala Val Ser Trp Val Ser Ala Lys Glu Ser Ala Thr Val Phe Thr Thr
515 520 525

Thr Ser Asn Gly Leu Ile Asp Val Thr Gly Leu Lys Tyr Gly Thr Tyr
530 535 540

Tyr Leu Glu Glu Thr Lys Ala Pro Glu Lys Tyr Val Pro Leu Thr Asn
545 550 555 560

Arg Val Ala Phe Thr Ile Asp Glu Gln Ser Tyr Val Thr Ala Gly Gln
565 570 575

Leu Ile Ser Pro Glu Lys Ile Pro Asn Lys His Lys Gly Thr Leu Pro
580 585 590

Ser Thr Gly Gly Lys Gly Ile Tyr Val Tyr Ile Gly Ala Gly Val Val
595 600 605

Leu Leu Leu Ile Ala Gly Leu Tyr Phe Ala Arg Arg Lys His Ser Gln
610 615 620

P07741US01_6-19-06_Sequence.txt

Ile
625

<210> 20

<211> 2402

<212> PRT

<213> Staphylococcus epidermidis

<400> 20

Met Lys Asn Lys Gln Gly Phe Leu Pro Asn Leu Leu Asn Lys Tyr Gly
1 5 10 15

Ile Arg Lys Leu Ser Ala Gly Thr Ala Ser Leu Leu Ile Gly Ala Thr
20 25 30

Leu Val Phe Gly Ile Asn Gly Gln Val Lys Ala Ala Glu Thr Asp Asn
35 40 45

Ile Val Ser Gln Asn Gly Asp Asn Lys Thr Asn Asp Ser Glu Ser Ser
50 55 60

Asp Lys Glu Leu Val Lys Ser Glu Asp Asp Lys Thr Ser Ser Thr Ser
65 70 75 80

Thr Asp Thr Asn Leu Glu Ser Glu Phe Asp Gln Asn Asn Asn Pro Ser
85 90 95

Ser Ile Glu Glu Ser Thr Asn Arg Asn Asp Glu Asp Thr Leu Asn Gln
100 105 110

Arg Thr Ser Thr Glu Thr Glu Lys Asp Thr His Val Lys Ser Ala Asp
115 120 125

Thr Gln Thr Thr Asn Glu Thr Thr Asn Lys Asn Asp Asp Asn Ala Thr
130 135 140

Thr Asn His Thr Glu Ser Ile Ser Asp Glu Ser Thr Tyr Gln Ser Asp
145 150 155 160

P07741US01_6-19-06_Sequence.txt

Asp Ser Lys Thr Thr Gln His Asp Asn Ser Asn Thr Asn Gln Asp Thr
165 170 175

Gln Ser Thr Leu Asn Pro Thr Ser Lys Glu Ser Ser Asn Lys Asp Glu
180 185 190

Ala Thr Ser Pro Thr Pro Lys Glu Ser Thr Ser Ile Glu Lys Thr Asn
195 200 205

Leu Ser Asn Asp Ala Asn His Gln Thr Thr Asp Glu Val Asn His Ser
210 215 220

Asp Ser Asp Asn Met Thr Asn Ser Thr Pro Asn Asp Thr Glu Asn Glu
225 230 235 240

Leu Asp Thr Thr Gln Leu Thr Ser His Asp Glu Ser Pro Ser Pro Gln
245 250 255

Ser Asp Asn Phe Thr Gly Phe Thr Asn Leu Met Ala Thr Pro Leu Asn
260 265 270

Leu Arg Asn Asp Asn Pro Arg Ile Asn Leu Leu Ala Ala Thr Glu Asp
275 280 285

Thr Lys Pro Lys Thr Tyr Lys Lys Pro Asn Asn Ser Glu Tyr Ser Tyr
290 295 300

Leu Leu Asn Asp Leu Gly Tyr Asp Ala Thr Thr Val Lys Glu Asn Ser
305 310 315 320

Asp Leu Arg His Ala Gly Ile Ser Gln Ser Gln Asp Asn Thr Gly Ser
325 330 335

Val Ile Lys Leu Asn Leu Thr Lys Trp Leu Ser Leu Gln Ser Asp Phe
340 345 350

Val Asn Gly Gly Lys Val Asn Leu Ser Phe Ala Gln Ser Asp Phe Tyr
355 360 365

P07741US01_6-19-06_Sequence.txt

Thr Gln Ile Glu Ser Ile Thr Leu Asn Asp Val Lys Met Asp Thr Thr
370 375 380

Asn Asn Gly Gln Asn Trp Ser Ala Pro Ile Asn Gly Ser Thr Val Arg
385 390 395 400

Ser Gly Leu Ile Gly Ser Val Thr Asn His Asp Ile Val Ile Thr Leu
405 410 415

Lys Asn Ser Gln Thr Leu Ser Ser Leu Gly Tyr Ser Asn Asn Lys Pro
420 425 430

Val Tyr Leu Thr His Thr Trp Thr Thr Asn Asp Gly Ala Ile Ala Glu
435 440 445

Glu Ser Ile Gln Val Ala Ser Ile Thr Pro Thr Leu Asp Ser Lys Ala
450 455 460

Pro Asn Thr Ile Gln Lys Ser Asp Phe Thr Ala Gly Arg Met Thr Asn
465 470 475 480

Lys Ile Lys Tyr Asp Ser Ser Gln Asn Ser Ile Lys Ser Val His Thr
485 490 495

Phe Lys Pro Asn Glu Asn Phe Leu Gln Thr Asp Tyr Arg Ala Val Leu
500 505 510

Tyr Ile Lys Glu Gln Val Asn Lys Glu Leu Ile Pro Tyr Ile Asp Pro
515 520 525

Asn Ser Val Lys Leu Tyr Val Ser Asp Pro Asp Gly Asn Pro Ile Ser
530 535 540

Gln Asp Arg Tyr Val Asn Gly Ser Ile Asp Asn Asp Gly Leu Phe Asp
545 550 555 560

Ser Ser Lys Ile Asn Glu Ile Ser Ile Lys Asn Asn Asn Thr Ser Gly
565 570 575

P07741US01_6-19-06_Sequence.txt

Gln Leu Ser Asn Ala Arg Thr Ser Leu Asp Arg Asn Val Phe Phe Gly
580 585 590

Thr Leu Gly Gln Ser Arg Ser Tyr Thr Ile Ser Tyr Lys Leu Lys Asp
595 600 605

Gly Tyr Thr Leu Glu Ser Val Ala Ser Lys Val Ser Ala Arg Glu Thr
610 615 620

Phe Asp Ser Trp Met Glu Val Asp Tyr Leu Asp Ser Tyr Asp Ser Gly
625 630 635 640

Ala Pro Asn Lys Arg Leu Leu Gly Ser Tyr Ala Ser Ser Tyr Ile Asp
645 650 655

Met Ile Asp Arg Ile Pro Pro Val Ala Pro Lys Ala Asn Ser Ile Thr
660 665 670

Thr Glu Asp Thr Ser Ile Lys Gly Thr Ala Glu Val Asp Thr Asn Ile
675 680 685

Asn Leu Thr Phe Asn Asp Gly Arg Thr Leu Asn Gly Lys Val Asp Ser
690 695 700

Asn Gly Asn Phe Ser Ile Ala Ile Pro Ser Tyr Tyr Val Leu Thr Gly
705 710 715 720

Lys Glu Thr Ile Lys Ile Thr Ser Ile Asp Lys Gly Asp Asn Val Ser
725 730 735

Pro Ala Ile Thr Ile Ser Val Ile Asp Lys Thr Pro Pro Ala Val Lys
740 745 750

Ala Ile Ser Asn Lys Thr Gln Lys Val Asn Thr Glu Ile Glu Pro Ile
755 760 765

Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val
770 775 780

P07741US01_6-19-06_Sequence.txt

Glu Gly Leu Pro Ala Gly Met Thr Phe Asp Glu Ala Thr Asn Thr Ile
785 790 795 800

Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr
805 810 815

Thr Asp Glu Asn Gly Asn Ser Glu Thr Thr Thr Phe Thr Ile Asp Val
820 825 830

Glu Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp Gln Thr Gln
835 840 845

Glu Val Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr Asp Asn
850 855 860

Ser Gly Arg Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asp Gly Val
865 870 875 880

Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val
885 890 895

Gly Ser Tyr Asp Ile Thr Val Thr Thr Asp Glu Ser Gly Asn Val
900 905 910

Thr Glu Thr Ile Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro Thr
915 920 925

Val Glu Ser Ile Ala Gly Gln Thr Gln Glu Val Asn Thr Glu Ile Glu
930 935 940

Pro Ile Lys Ile Glu Ala Lys Asp Asn Ser Gly Gln Thr Val Thr Asn
945 950 955 960

Lys Val Asp Gly Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr Asn
965 970 975

Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Val Thr Val
980 985 990

P07741US01_6-19-06_Sequence.txt

Thr Thr Thr Asp Glu Ser Gly Asn Ser Glu Thr Thr Thr Phe Thr Ile
995 1000 1005

Glu Val Lys Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp
1010 1015 1020

Gln Thr Gln Glu Val Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu
1025 1030 1035

Ala Arg Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val Asp Gly
1040 1045 1050

Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser
1055 1060 1065

Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr
1070 1075 1080

Thr Asp Glu Ser Gly Asn Val Thr Glu Thr Thr Phe Thr Ile Glu
1085 1090 1095

Val Glu Asp Thr Thr Lys Pro Thr Val Glu Asn Val Ala Asp Gln
1100 1105 1110

Thr Gln Glu Val Asn Thr Glu Ile Thr Pro Ile Thr Ile Glu Ser
1115 1120 1125

Glu Asp Asn Ser Gly Gln Thr Val Thr Asn Lys Val Asp Gly Leu
1130 1135 1140

Pro Asp Gly Val Thr Phe Asp Glu Thr Thr Asn Thr Ile Ser Gly
1145 1150 1155

Thr Pro Ser Lys Val Gly Ser Tyr Asp Ile Thr Val Thr Thr Thr
1160 1165 1170

Asp Glu Ser Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Glu Val
1175 1180 1185

P07741US01_6-19-06_Sequence.txt

Glu Asp Thr Thr Lys Pro Thr Val Glu Asn Val Ala Gly Gln Thr
1190 1195 1200

Gln Glu Ile Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr
1205 1210 1215

Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val Glu Gly Leu Pro
1220 1225 1230

Ala Gly Val Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr
1235 1240 1245

Pro Ser Glu Val Gly Ser Tyr Thr Val Thr Val Thr Thr Met Asp
1250 1255 1260

Glu Ser Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Asp Val Glu
1265 1270 1275

Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp Gln Thr Gln
1280 1285 1290

Glu Val Asn Thr Glu Ile Thr Pro Ile Thr Ile Glu Ser Glu Asp
1295 1300 1305

Asn Ser Asp Gln Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asp
1310 1315 1320

Gly Val Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro
1325 1330 1335

Ser Glu Val Gly Ser Tyr Thr Val Thr Val Thr Thr Asp Glu
1340 1345 1350

Ser Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Asp Val Glu Asp
1355 1360 1365

Thr Thr Lys Pro Thr Val Lys Ser Val Ser Asp Gln Thr Gln Glu
1370 1375 1380

P07741US01_6-19-06_Sequence.txt

Val Asn Thr Glu Ile Thr Pro Ile Lys Ile Glu Ala Thr Asp Asn
1385 1390 1395

Ser Gly Gln Thr Val Thr Asn Lys Val Asp Gly Leu Pro Asp Gly
1400 1405 1410

Ile Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser
1415 1420 1425

Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr Thr Asp Glu Ser
1430 1435 1440

Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Asn Val Glu Asp Thr
1445 1450 1455

Thr Lys Pro Thr Val Glu Asp Ile Ala Asp Gln Thr Gln Glu Val
1460 1465 1470

Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr Asp Asn Gly
1475 1480 1485

Gly Gln Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asp Gly Val
1490 1495 1500

Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu
1505 1510 1515

Val Gly Ser Tyr Asp Ile Ile Val Thr Thr Thr Asp Glu Asn Gly
1520 1525 1530

Asn Ser Glu Thr Thr Phe Thr Ile Asp Val Glu Asp Thr Thr
1535 1540 1545

Lys Pro Thr Val Glu Ser Val Val Asp Gln Thr Gln Glu Val Asn
1550 1555 1560

Thr Glu Ile Thr Pro Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly
1565 1570 1575

P07741US01_6-19-06_Sequence.txt

Gln Ala Val Ala Asn Lys Val Asp Gly Leu Pro Asn Gly Val Thr
1580 1585 1590

Phe Asp Glu Thr Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val
1595 1600 1605

Gly Ser Tyr Asp Ile Ile Val Thr Thr Thr Asp Glu Ser Gly Asn
1610 1615 1620

Val Thr Glu Thr Ile Phe Thr Ile Asp Val Glu Asp Thr Thr Lys
1625 1630 1635

Pro Thr Val Glu Ser Ile Ala Gly Gln Thr Gln Glu Val Asn Thr
1640 1645 1650

Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln
1655 1660 1665

Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asn Gly Val Thr Phe
1670 1675 1680

Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly
1685 1690 1695

Ile Tyr Thr Val Thr Val Thr Thr Asp Glu Ser Gly Asn Ala
1700 1705 1710

Thr Glu Thr Thr Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro
1715 1720 1725

Thr Val Glu Ser Val Ala Asp Gln Thr Gln Glu Val Asn Thr Glu
1730 1735 1740

Ile Thr Pro Ile Thr Ile Glu Ser Glu Asp Asn Ser Gly Gln Ala
1745 1750 1755

Val Thr Asn Lys Val Glu Gly Leu Pro Ala Gly Met Thr Phe Asp
1760 1765 1770

P07741US01_6-19-06_Sequence.txt

Glu Thr Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser
1775 1780 1785

Tyr Thr Val Thr Val Thr Thr Asp Glu Ser Gly Asn Glu Thr
1790 1795 1800

Glu Thr Thr Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro Thr
1805 1810 1815

Val Glu Ser Ile Ala Asn Gln Thr Gln Glu Val Asn Thr Glu Ile
1820 1825 1830

Thr Pro Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln Ala Val
1835 1840 1845

Thr Asn Lys Val Asp Gly Leu Pro Asn Gly Val Thr Phe Asp Glu
1850 1855 1860

Thr Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr
1865 1870 1875

Asp Ile Lys Val Thr Thr Asp Glu Ser Gly Asn Ala Thr Glu
1880 1885 1890

Thr Thr Phe Thr Ile Asn Val Glu Asp Thr Thr Lys Pro Thr Val
1895 1900 1905

Glu Ser Val Ala Asp Gln Thr Gln Glu Ile Asn Thr Glu Ile Glu
1910 1915 1920

Pro Ile Lys Ile Glu Ala Arg Asp Asn Ser Gly Gln Ala Val Thr
1925 1930 1935

Asn Lys Val Asp Gly Leu Pro Asp Gly Val Thr Phe Asp Glu Ala
1940 1945 1950

Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp
1955 1960 1965

P07741US01_6-19-06_Sequence.txt

Ile Thr Val Thr Thr Asp Glu Ser Gly Asn Ala Thr Glu Thr
1970 1975 1980

Thr Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro Thr Val Glu
1985 1990 1995

Asp Ile Thr Asp Gln Thr Gln Glu Ile Asn Thr Glu Met Thr Pro
2000 2005 2010

Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln Ala Val Thr Asn
2015 2020 2025

Lys Val Glu Gly Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr
2030 2035 2040

Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Lys Tyr Leu Ile
2045 2050 2055

Thr Ile Thr Thr Ile Asp Lys Asp Gly Asn Thr Ala Thr Thr Thr
2060 2065 2070

Leu Thr Ile Asn Val Ile Asp Thr Thr Thr Pro Glu Gln Pro Thr
2075 2080 2085

Ile Asn Lys Val Thr Glu Asn Ser Thr Glu Val Asn Gly Arg Gly
2090 2095 2100

Glu Pro Gly Thr Val Val Glu Val Thr Phe Pro Asp Gly Asn Lys
2105 2110 2115

Val Glu Gly Lys Val Asp Ser Asp Gly Asn Tyr His Ile Gln Ile
2120 2125 2130

Pro Ser Glu Thr Thr Leu Lys Gly Gly Gln Pro Leu Gln Val Ile
2135 2140 2145

Ala Ile Asp Lys Ala Gly Asn Lys Ser Glu Ala Thr Thr Thr Asn
2150 2155 2160

P07741US01_6-19-06_Sequence.txt

Val Ile Asp Thr Thr Ala Pro Glu Gln Pro Thr Ile Asn Lys Val
2165 2170 2175

Thr Glu Asn Ser Thr Glu Val Ser Gly Arg Gly Glu Pro Gly Thr
2180 2185 2190

Val Val Glu Val Thr Phe Pro Asp Gly Asn Lys Val Glu Gly Lys
2195 2200 2205

Val Asp Ser Asp Gly Asn Tyr His Ile Gln Ile Pro Ser Asp Glu
2210 2215 2220

Arg Phe Lys Val Gly Gln Gln Leu Ile Val Lys Val Val Asp Glu
2225 2230 2235

Glu Gly Asn Val Ser Glu Pro Ser Ile Thr Met Val Gln Lys Glu
2240 2245 2250

Asp Lys Asn Ser Glu Lys Leu Ser Thr Val Thr Gly Thr Val Thr
2255 2260 2265

Lys Asn Asn Ser Lys Ser Leu Lys His Lys Ala Ser Glu Gln Gln
2270 2275 2280

Ser Tyr His Asn Lys Ser Glu Lys Ile Lys Asn Val Asn Lys Pro
2285 2290 2295

Thr Lys Ile Val Glu Lys Asp Met Ser Thr Tyr Asp Tyr Ser Arg
2300 2305 2310

Tyr Ser Lys Asp Ile Ser Asn Lys Asn Asn Lys Ser Ala Thr Phe
2315 2320 2325

Glu Gln Gln Asn Val Ser Asp Ile Asn Asn Asn Gln Tyr Ser Arg
2330 2335 2340

Asn Lys Val Asn Gln Pro Val Lys Lys Ser Arg Lys Asn Glu Ile
2345 2350 2355

P07741US01_6-19-06_Sequence.txt

Asn Lys Asp Leu Pro Gln Thr Gly Glu Glu Asn Phe Asn Lys Ser
2360 2365 2370

Thr Leu Phe Gly Thr Leu Val Ala Ser Leu Gly Ala Leu Leu Leu
2375 2380 2385

Phe Phe Lys Arg Arg Lys Lys Asp Glu Asn Asp Glu Lys Glu
2390 2395 2400

<210> 21

<211> 892

<212> PRT

<213> Staphylococcus epidermidis

<400> 21

Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Thr Val
1 5 10 15

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20 25 30

Asp Gln Ser Ser Asn Glu Glu Lys Asn Asp Val Ile Asn Asn Ser Gln
35 40 45

Ser Ile Asn Thr Asp Asp Asp Asn Gln Ile Lys Lys Glu Glu Thr Asn
50 55 60

Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys Asp Ile Thr Gln Ser Thr
65 70 75 80

Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln
85 90 95

Asp Asn Thr Gln Leu Lys Glu Glu Val Val Lys Glu Pro Ser Ser Val
100 105 110

Glu Ser Ser Asn Ser Ser Met Asp Thr Ala Gln Gln Pro Ser His Thr
115 120 125

Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr Ser Asp Asn Glu Glu Asn

P07741US01_6-19-06_Sequence.txt

130

135

140

Ser Arg Val Ser Asp Phe Ala Asn Ser Lys Ile Ile Glu Ser Asn Thr
145 150 155 160

Glu Ser Asn Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Arg
165 170 175

Glu Asp Ser Ile Thr Ser Gln Pro Ser Ser Tyr Lys Asn Ile Asp Glu
180 185 190

Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr
195 200 205

Glu Asn Lys Val Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ser
210 215 220

Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val
225 230 235 240

Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp
245 250 255

Asp Ser Asp Gly Ile Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr
260 265 270

Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met
275 280 285

Thr Val Asn Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser
290 295 300

Phe Ala Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr
305 310 315 320

Gly Thr Tyr Asp Asn Thr Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp
325 330 335

Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser
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P07741US01_6-19-06_Sequence.txt

340

345

350

Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val
355 360 365

Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu
370 375 380

Tyr Gln Lys Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe
385 390 395 400

Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile
405 410 415

Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly
420 425 430

Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys
435 440 445

Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile
450 455 460

Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln
465 470 475 480

Leu Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser
485 490 495

Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp
500 505 510

Tyr Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu
515 520 525

Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe
530 535 540

Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr
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P07741US01_6-19-06_Sequence.txt

545

550

555

560

Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile
565 570 575

Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr
580 585 590

Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Glu
595 600 605

Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr Lys Ile
610 615 620

Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His Ser Gly
625 630 635 640

Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val Thr Ile
645 650 655

Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln Thr Pro
660 665 670

Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys Asp Gly
675 680 685

Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val Thr Leu
690 695 700

Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Thr Asp Glu Asn
705 710 715 720

Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile Val His
725 730 735

Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser Gly Asp
740 745 750

Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr Ile Thr
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P07741US01_6-19-06_Sequence.txt

755

760

765

Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp Asp Ser
 770 775 780

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Asp Ser Asp Ser Asp Asp
 785 790 795 800

Ser Asp
 805 810 815

Ser Asp
 820 825 830

Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp Asn Ser Ser Asp Lys Asn
 835 840 845

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser
 850 855 860

Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala Gly Leu Gly Ala Leu Leu
 865 870 875 880

Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn
 885 890

<210> 22

<211> 1973

<212> PRT

<213> Staphylococcus epidermidis

<400> 22

Met Lys Glu Asn Lys Arg Lys Asn Asn Leu Asp Lys Asn Asn Thr Arg
 1 5 10 15

Phe Ser Ile Arg Lys Tyr Gln Gly Tyr Gly Ala Thr Ser Val Ala Ile
 20 25 30

Ile Gly Phe Ile Ile Ser Cys Phe Ser Glu Ala Lys Ala Asp Ser
 35 40 45

P07741US01_6-19-06_Sequence.txt

Asp Lys His Glu Ile Lys Ser His Gln Gln Ser Met Thr Asn His Leu
50 55 60

Thr Thr Leu Pro Ser Asp Asn Gln Glu Asn Thr Ser Asn Asn Glu Phe
65 70 75 80

Asn Asn Arg Asn His Asp Ile Ser His Leu Ser Leu Asn Lys Ser Ile
85 90 95

Gln Met Asp Glu Leu Lys Lys Leu Ile Lys Gln Tyr Lys Ala Ile Asn
100 105 110

Leu Asn Asp Lys Thr Glu Glu Ser Ile Lys Leu Phe Gln Ser Asp Leu
115 120 125

Val Gln Ala Glu Ser Leu Ile Asn Asn Pro Gln Ser Gln Gln His Val
130 135 140

Asp Ala Phe Tyr His Lys Phe Leu Asn Ser Ala Gly Lys Leu Arg Lys
145 150 155 160

Lys Glu Thr Val Ser Ile Lys His Glu Arg Ser Glu Ser Asn Thr Tyr
165 170 175

Arg Leu Gly Asp Glu Val Arg Ser Gln Thr Phe Ser His Ile Arg His
180 185 190

Lys Arg Asn Ala Val Ser Phe Arg Asn Ala Asp Gln Ser Asn Leu Ser
195 200 205

Thr Asp Pro Leu Lys Ala Asn Glu Ile Asn Pro Glu Ile Gln Asn Gly
210 215 220

Asn Phe Ser Gln Val Ser Gly Gly Pro Leu Pro Thr Ser Ser Lys Arg
225 230 235 240

Leu Thr Val Val Thr Asn Val Asp Asn Trp His Ser Tyr Ser Thr Asp
245 250 255

P07741US01_6-19-06_Sequence.txt

Pro Asn Pro Glu Tyr Pro Met Phe Tyr Thr Thr Thr Ala Val Asn Tyr
260 265 270

Pro Asn Phe Met Ser Asn Gly Asn Ala Pro Tyr Gly Val Ile Leu Gly
275 280 285

Arg Thr Thr Asp Gly Trp Asn Arg Asn Val Ile Asp Ser Lys Val Ala
290 295 300

Gly Ile Tyr Gln Asp Ile Asp Val Val Pro Gly Ser Glu Leu Asn Val
305 310 315 320

Asn Phe Ile Ser Thr Ser Pro Val Phe Ser Asp Gly Ala Ala Gly Ala
325 330 335

Lys Leu Lys Ile Ser Asn Val Glu Gln Asn Arg Val Leu Phe Asp Ser
340 345 350

Arg Leu Asn Gly Met Gly Pro Tyr Pro Thr Gly Lys Leu Ser Ala Met
355 360 365

Val Asn Ile Pro Asn Asp Ile Asn Arg Val Arg Ile Ser Phe Leu Pro
370 375 380

Val Ser Ser Thr Gly Arg Val Ser Val Gln Arg Ser Ser Arg Glu His
385 390 395 400

Gly Phe Gly Asp Asn Ser Ser Tyr Tyr His Gly Gly Ser Val Ser Asp
405 410 415

Val Arg Ile Asn Ser Gly Ser Tyr Val Val Ser Lys Val Thr Gln Arg
420 425 430

Glu Tyr Thr Thr Arg Pro Asn Ser Ser Asn Asp Thr Phe Ala Arg Ala
435 440 445

Thr Ile Asn Leu Ser Val Glu Asn Lys Gly His Asn Gln Ser Lys Asp
450 455 460

P07741US01_6-19-06_Sequence.txt

Thr Tyr Tyr Glu Val Ile Leu Pro Gln Asn Ser Arg Leu Ile Ser Thr
465 470 475 480

Arg Gly Gly Ser Gly Asn Tyr Asn Asn Ala Thr Asn Lys Leu Ser Ile
485 490 495

Arg Leu Asp Asn Leu Asn Pro Gly Asp Arg Arg Asp Ile Ser Tyr Thr
500 505 510

Val Asp Phe Glu Ser Ser Ser Pro Lys Leu Ile Asn Leu Asn Ala His
515 520 525

Leu Leu Tyr Lys Thr Asn Ala Thr Phe Arg Gly Asn Asp Gly Gln Arg
530 535 540

Thr Gly Asp Asn Ile Val Asp Leu Gln Ser Ile Ala Leu Leu Met Asn
545 550 555 560

Lys Asp Val Leu Glu Thr Glu Leu Asn Glu Ile Asp Lys Phe Ile Arg
565 570 575

Asp Leu Asn Glu Ala Asp Phe Thr Ile Asp Ser Trp Ser Ala Leu Gln
580 585 590

Glu Lys Met Thr Glu Gly Asn Ile Leu Asn Glu Gln Gln Asn Gln
595 600 605

Val Ala Leu Glu Asn Gln Ala Ser Gln Glu Thr Ile Asn Asn Val Thr
610 615 620

Gln Ser Leu Glu Ile Leu Lys Asn Asn Leu Lys Tyr Lys Thr Pro Ser
625 630 635 640

Gln Pro Ile Ile Lys Ser Asn Asn Gln Ile Pro Asn Ile Thr Ile Ser
645 650 655

Pro Ala Asp Lys Ala Asp Lys Leu Thr Ile Thr Tyr Gln Asn Thr Asp
660 665 670

P07741US01_6-19-06_Sequence.txt

Asn Glu Ser Ala Ser Ile Ile Gly Asn Lys Leu Asn Asn Gln Trp Ser
675 680 685

Leu Asn Asn Asn Ile Pro Gly Ile Glu Ile Asp Met Gln Thr Gly Leu
690 695 700

Val Thr Ile Asp Tyr Lys Ala Val Tyr Pro Glu Ser Val Val Gly Ala
705 710 715 720

Asn Asp Lys Thr Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr
725 730 735

Met Pro Arg Lys Glu Ala Thr Pro Leu Ser Pro Ile Val Glu Ala Asn
740 745 750

Glu Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln
755 760 765

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu Val
770 775 780

Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile Asp Tyr
785 790 795 800

Val Asn Ile Glu Glu Asn Ser Gly Lys Val Thr Ile Gly Tyr Gln Ala
805 810 815

Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr Lys Gly Asn Ser
820 825 830

Asp Glu Ser Ala Glu Ser Arg Val Thr Met Pro Arg Lys Glu Ala Thr
835 840 845

Pro His Ser Pro Ile Val Glu Ala Asn Glu Glu His Val Asn Val Thr
850 855 860

Ile Ala Pro Asn Gly Glu Ala Thr Gln Ile Ala Ile Lys Tyr Arg Thr
865 870 875 880

P07741US01_6-19-06_Sequence.txt

Pro Asp Gly Gln Glu Thr Thr Leu Ile Ala Ser Lys Asn Gly Ser Ser
885 890 895

Trp Thr Leu Asn Lys Gln Ile Asp Tyr Val Asn Ile Glu Glu Asn Ser
900 905 910

Gly Lys Val Thr Ile Gly Tyr Gln Ala Val Gln Leu Glu Ser Glu Val
915 920 925

Ile Ala Thr Glu Thr Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg
930 935 940

Ile Thr Met Leu Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu
945 950 955 960

Ala Asn Glu Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Ala
965 970 975

Thr Gln Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr
980 985 990

Leu Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
995 1000 1005

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1010 1015 1020

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr
1025 1030 1035

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1040 1045 1050

Arg Lys Glu Ala Thr Pro Ile Pro Pro Thr Leu Glu Ala Ser Val
1055 1060 1065

Gln Glu Ala Ser Val Thr Val Thr Pro Asn Glu Asn Ala Thr Lys
1070 1075 1080

P07741US01_6-19-06_Sequence.txt

val Phe Ile Lys Tyr Leu Asp Ile Asn Asp Glu Ile Ser Thr Ile
1085 1090 1095

Ile Ala Ser Lys Ile Asn Gln Gln Trp Thr Leu Asn Lys Asp Asn
1100 1105 1110

Phe Gly Ile Lys Ile Asn Pro Leu Thr Gly Lys Val Ile Ile Ser
1115 1120 1125

Tyr val Ala Val Gln Pro Glu Ser Asp Val Ile Ala Ile Glu Ser
1130 1135 1140

Gln Gly Asn Ser Asp Leu Ser Glu Glu Ser Arg Ile Ile Met Pro
1145 1150 1155

Thr Lys Glu Glu Pro Pro Glu Pro Pro Ile Leu Glu Ser Asp Ser
1160 1165 1170

Ile Glu Ala Lys Val Asn Ile Phe Pro Asn Asp Glu Ala Thr Arg
1175 1180 1185

Ile val Ile Met Tyr Thr Ser Leu Glu Gly Gln Glu Ala Thr Leu
1190 1195 1200

val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
1205 1210 1215

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1220 1225 1230

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr
1235 1240 1245

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Val Thr Met Pro
1250 1255 1260

Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu Thr Asn Glu
1265 1270 1275

P07741US01_6-19-06_Sequence.txt

Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln
1280 1285 1290

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Thr Thr Leu
1295 1300 1305

Ile Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile
1310 1315 1320

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1325 1330

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr
1340 1345 1350

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1355 1360 1365

Arg Lys Glu Ala Ile Pro His Ser Pro Ile Val Glu Ala Asn Glu
1370 1375 1380

Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Thr Thr Gln
1385 1390 1395

Ile Ala Val Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu
1400 1405 1410

Ile Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
1415 1420 1425

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1430 1435 1440

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr
1445 1450 1455

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1460 1465 1470

P07741US01_6-19-06_Sequence.txt

Val Lys Glu Lys Thr Pro Ala Pro Pro Ile Ser Ile Ile Asn Glu
1475 1480 1485

Ser Asn Ala Ser Val Glu Ile Ile Pro Gln Val Asn Val Thr Gln
1490 1495 1500

Leu Ser Leu Gln Tyr Ile Asp Ala Lys Gly Gln Gln Gln Asn Leu
1505 1510 1515

Ile Ala Thr Leu Asn Gln Asn Gln Trp Thr Leu Asn Lys Asn Val
1520 1525 1530

Ser His Ile Thr Val Asp Lys Asn Thr Gly Lys Val Leu Ile Asn
1535 1540 1545

Tyr Gln Ala Val Tyr Pro Glu Ser Glu Val Ile Ala Arg Glu Ser
1550 1555 1560

Lys Gly Asn Ser Asp Ser Ser Asn Val Ser Met Val Ile Met Pro
1565 1570 1575

Arg Lys Thr Ala Thr Pro Lys Pro Pro Ile Ile Lys Val Asp Glu
1580 1585 1590

Met Asn Ala Ser Leu Ala Ile Ile Pro Tyr Lys Asn Asn Thr Ala
1595 1600 1605

Ile Asn Ile His Tyr Ile Asp Lys Lys Gly Ile Lys Ser Met Val
1610 1615 1620

Thr Ala Ile Lys Asn Asn Asp Gln Trp Gln Leu Asp Glu Lys Ile
1625 1630 1635

Lys Tyr Val Lys Ile Asp Ala Lys Thr Gly Thr Val Ile Ile Asn
1640 1645 1650

Tyr Gln Ile Val Gln Glu Asn Ser Glu Ile Ile Ala Thr Ala Ile
1655 1660 1665

P07741US01_6-19-06_Sequence.txt

Asn Gly Asn Ser Asp Lys Ser Glu Glu Val Lys Val Leu Met Pro
1670 1675 1680

Ile Lys Glu Phe Thr Pro Leu Ala Pro Leu Leu Glu Thr Asn Tyr
1685 1690 1695

Lys Lys Ala Thr Val Ser Ile Leu Pro Gln Ser Asn Ala Thr Lys
1700 1705 1710

Leu Asp Phe Lys Tyr Arg Asp Lys Lys Gly Asp Ser Lys Ile Ile
1715 1720 1725

Ile Val Lys Arg Phe Lys Asn Ile Trp Lys Ala Asn Glu Gln Ile
1730 1735 1740

Ser Gly Val Thr Ile Asn Pro Glu Phe Gly Gln Val Val Ile Asn
1745 1750 1755

Tyr Gln Ala Val Tyr Pro Glu Ser Asp Ile Leu Ala Ala Gln Tyr
1760 1765 1770

Val Gly Asn Ser Asp Ala Ser Glu Trp Ala Lys Val Lys Met Pro
1775 1780 1785

Lys Lys Glu Leu Ala Pro His Ser Pro Ser Leu Ile Tyr Asp Asn
1790 1795 1800

Arg Asn Asn Lys Ile Leu Ile Ala Pro Asn Ser Asn Ala Thr Glu
1805 1810 1815

Met Glu Leu Ser Tyr Val Asp Lys Asn Asn Gln Ser Leu Lys Val
1820 1825 1830

Lys Ala Leu Lys Ile Asn Asn Arg Trp Lys Phe Asp Ser Ser Val
1835 1840 1845

Ser Asn Ile Ser Ile Asn Pro Asn Thr Gly Lys Ile Val Leu Gln
1850 1855 1860

P07741US01_6-19-06_Sequence.txt

Pro Gln Phe Leu Leu Thr Asn Ser Lys Ile Ile Val Phe Ala Lys
1865 1870 1875

Lys Gly Asn Ser Asp Ala Ser Ile Ser Val Ser Leu Arg Val Pro
1880 1885 1890

Ala Val Lys Lys Ile Glu Leu Glu Pro Met Phe Asn Val Pro Val
1895 1900 1905

Leu Val Ser Leu Asn Lys Lys Arg Ile Gln Phe Asp Asp Cys Ser
1910 1915 1920

Gly Val Lys Asn Cys Leu Asn Lys Gln Ile Ser Lys Thr Gln Leu
1925 1930 1935

Pro Asp Thr Gly Tyr Ser Asp Lys Ala Ser Lys Ser Asn Ile Leu
1940 1945 1950

Ser Val Leu Leu Leu Gly Phe Gly Phe Leu Ser Tyr Ser Arg Lys
1955 1960 1965

Arg Lys Glu Lys Gln
1970

<210> 23

<211> 10203

<212> PRT

<213> Staphylococcus epidermidis

<400> 23

Met Lys Ser Lys Pro Lys Leu Asn Gly Arg Asn Ile Cys Ser Phe Leu
1 5 10 15

Leu Ser Lys Cys Met Ser Tyr Ser Leu Ser Lys Leu Ser Thr Leu Lys
20 25 30

Thr Tyr Asn Phe Gln Ile Thr Ser Asn Asn Lys Glu Lys Thr Ser Arg
35 40 45

P07741US01_6-19-06_Sequence.txt

Ile Gly Val Ala Ile Ala Leu Asn Asn Arg Asp Lys Leu Gln Lys Phe
50 55 60

Ser Ile Arg Lys Tyr Ala Ile Gly Thr Phe Ser Thr Val Ile Ala Thr
65 70 75 80

Leu Val Phe Met Gly Ile Asn Thr Asn His Ala Ser Ala Asp Glu Leu
85 90 95

Asn Gln Asn Gln Lys Leu Ile Lys Gln Leu Asn Gln Thr Asp Asp Asp
100 105 110

Asp Ser Asn Thr His Ser Gln Glu Ile Glu Asn Asn Lys Gln Asn Ser
115 120 125

Ser Gly Lys Thr Glu Ser Leu Arg Ser Ser Thr Ser Gln Asn Gln Ala
130 135 140

Asn Ala Arg Leu Ser Asp Gln Phe Lys Asp Thr Asn Glu Thr Ser Gln
145 150 155 160

Gln Leu Pro Thr Asn Val Ser Asp Asp Ser Ile Asn Gln Ser His Ser
165 170 175

Glu Ala Asn Met Asn Asn Glu Pro Leu Lys Val Asp Asn Ser Thr Met
180 185 190

Gln Ala His Ser Lys Ile Val Ser Asp Ser Asp Gly Asn Ala Ser Glu
195 200 205

Asn Lys His His Lys Leu Thr Glu Asn Val Leu Ala Glu Ser Arg Ala
210 215 220

Ser Lys Asn Asp Lys Glu Lys Glu Asn Leu Gln Glu Lys Asp Lys Ser
225 230 235 240

Gln Gln Val His Pro Pro Leu Asp Lys Asn Ala Leu Gln Ala Phe Phe
245 250 255

P07741US01_6-19-06_Sequence.txt

Asp Ala Ser Tyr His Asn Tyr Arg Met Ile Asp Arg Asp Arg Ala Asp
260 265 270

Ala Thr Glu Tyr Gln Lys Val Lys Ser Thr Phe Asp Tyr Val Asn Asp
275 280 285

Leu Leu Gly Asn Asn Gln Asn Ile Pro Ser Glu Gln Leu Val Ser Ala
290 295 300

Tyr Gln Gln Leu Glu Lys Ala Leu Glu Leu Ala Arg Thr Leu Pro Gln
305 310 315 320

Gln Ser Thr Thr Glu Lys Arg Gly Arg Arg Ser Thr Arg Ser Val Val
325 330 335

Glu Asn Arg Ser Ser Arg Ser Asp Tyr Leu Asp Ala Arg Thr Glu Tyr
340 345 350

Tyr Val Ser Lys Asp Asp Asp Asp Ser Gly Phe Pro Pro Gly Thr Phe
355 360 365

Phe His Ala Ser Asn Arg Arg Trp Pro Tyr Asn Leu Pro Arg Ser Arg
370 375 380

Asn Ile Leu Arg Ala Ser Asp Val Gln Gly Asn Ala Tyr Ile Thr Thr
385 390 395 400

Lys Arg Leu Lys Asp Gly Tyr Gln Trp Asp Ile Leu Phe Asn Ser Asn
405 410 415

His Lys Gly His Glu Tyr Met Tyr Tyr Trp Phe Gly Leu Pro Ser Asp
420 425 430

Gln Thr Pro Thr Gly Pro Val Thr Phe Thr Ile Ile Asn Arg Asp Gly
435 440 445

Ser Ser Thr Ser Thr Gly Gly Val Gly Phe Gly Ser Gly Ala Pro Leu
450 455 460

P07741US01_6-19-06_Sequence.txt

Pro Gln Phe Trp Arg Ser Ala Gly Ala Ile Asn Ser Ser Val Ala Asn
465 470 475 480

Asp Phe Lys His Gly Ser Ala Thr Asn Tyr Ala Phe Tyr Asp Gly Val
485 490 495

Asn Asn Phe Ser Asp Phe Ala Arg Gly Gly Glu Leu Tyr Phe Asp Arg
500 505 510

Glu Gly Ala Thr Gln Thr Asn Lys Tyr Tyr Gly Asp Glu Asn Phe Ala
515 520 525

Leu Leu Asn Ser Glu Lys Pro Asp Gln Ile Arg Gly Leu Asp Thr Ile
530 535 540

Tyr Ser Phe Lys Gly Ser Gly Asp Val Ser Tyr Arg Ile Ser Phe Lys
545 550 555 560

Thr Gln Gly Ala Pro Thr Ala Arg Leu Tyr Tyr Ala Ala Gly Ala Arg
565 570 575

Ser Gly Glu Tyr Lys Gln Ala Thr Asn Tyr Asn Gln Leu Tyr Val Glu
580 585 590

Pro Tyr Lys Asn Tyr Arg Asn Arg Val Gln Ser Asn Val Gln Val Lys
595 600 605

Asn Arg Thr Leu His Leu Lys Arg Thr Ile Arg Gln Phe Asp Pro Thr
610 615 620

Leu Gln Arg Thr Thr Asp Val Pro Ile Leu Asp Ser Asp Gly Ser Gly
625 630 635 640

Ser Ile Asp Ser Val Tyr Asp Pro Leu Ser Tyr Val Lys Asn Val Thr
645 650 655

Gly Thr Val Leu Gly Ile Tyr Pro Ser Tyr Leu Pro Tyr Asn Gln Glu
660 665 670

P07741US01_6-19-06_Sequence.txt

Arg Trp Gln Gly Ala Asn Ala Met Asn Ala Tyr Gln Ile Glu Glu Leu
675 680 685

Phe Ser Gln Glu Asn Leu Gln Asn Ala Ala Arg Ser Gly Arg Pro Ile
690 695 700

Gln Phe Leu Val Gly Phe Asp Val Glu Asp Ser His His Asn Pro Glu
705 710 715 720

Thr Leu Leu Pro Val Asn Leu Tyr Val Lys Pro Glu Leu Lys His Thr
725 730 735

Ile Glu Leu Tyr His Asp Asn Glu Lys Gln Asn Arg Lys Glu Phe Ser
740 745 750

Val Ser Lys Arg Ala Gly His Gly Val Phe Gln Ile Met Ser Gly Thr
755 760 765

Leu His Asn Thr Val Gly Ser Gly Ile Leu Pro Tyr Gln Gln Glu Ile
770 775 780

Arg Ile Lys Leu Thr Ser Asn Glu Pro Ile Lys Asp Ser Glu Trp Ser
785 790 795 800

Ile Thr Gly Tyr Pro Asn Thr Leu Thr Leu Gln Asn Ala Val Gly Arg
805 810 815

Thr Asn Asn Ala Thr Glu Lys Asn Leu Ala Leu Val Gly His Ile Asp
820 825 830

Pro Gly Asn Tyr Phe Ile Thr Val Lys Phe Gly Asp Lys Val Glu Gln
835 840 845

Phe Glu Ile Arg Ser Lys Pro Thr Pro Pro Arg Ile Ile Thr Thr Ala
850 855 860

Asn Glu Leu Arg Gly Asn Ser Asn His Lys Pro Glu Ile Arg Val Thr
865 870 875 880

P07741US01_6-19-06_Sequence.txt

Asp Ile Pro Asn Asp Thr Thr Ala Lys Ile Lys Leu Val Met Gly Gly
885 890 895

Thr Asp Gly Asp His Asp Pro Glu Ile Asn Pro Tyr Thr Val Pro Glu
900 905 910

Asn Tyr Thr Val Val Ala Glu Ala Tyr His Asp Asn Asp Pro Ser Lys
915 920 925

Asn Gly Val Leu Thr Phe Arg Ser Ser Asp Tyr Leu Lys Asp Leu Pro
930 935 940

Leu Ser Gly Glu Leu Lys Ala Ile Val Tyr Tyr Asn Gln Tyr Val Gln
945 950 955 960

Ser Asn Phe Ser Asn Ser Val Pro Phe Ser Ser Asp Thr Thr Pro Pro
965 970 975

Thr Ile Asn Glu Pro Ala Gly Leu Val His Lys Tyr Tyr Arg Gly Asp
980 985 990

His Val Glu Ile Thr Leu Pro Val Thr Asp Asn Thr Gly Gly Ser Gly
995 1000 1005

Leu Arg Asp Val Asn Val Asn Leu Pro Gln Gly Trp Thr Lys Thr
1010 1015 1020

Phe Thr Ile Asn Pro Asn Asn Asn Thr Glu Gly Thr Leu Lys Leu
1025 1030 1035

Ile Gly Asn Ile Pro Ser Asn Glu Ala Tyr Asn Thr Thr Tyr His
1040 1045 1050

Phe Asn Ile Thr Ala Thr Asp Asn Ser Gly Asn Thr Thr Asn Pro
1055 1060 1065

Ala Lys Thr Phe Ile Leu Asn Val Gly Lys Leu Ala Asp Asp Leu
1070 1075 1080

P07741US01_6-19-06_Sequence.txt

Asn Pro Val Gly Leu Ser Arg Asp Gln Leu Gln Leu Val Thr Asp
1085 1090 1095

Pro Ser Ser Leu Ser Asn Ser Glu Arg Glu Glu Val Lys Arg Lys
1100 1105 1110

Ile Ser Glu Ala Asn Ala Asn Ile Arg Ser Tyr Leu Leu Gln Asn
1115 1120 1125

Asn Pro Ile Leu Ala Gly Val Asn Gly Asp Val Thr Phe Tyr Tyr
1130 1135 1140

Arg Asp Gly Ser Val Asp Val Ile Asp Ala Glu Asn Val Ile Thr
1145 1150 1155

Tyr Glu Pro Glu Arg Lys Ser Ile Phe Ser Glu Asn Gly Asn Thr
1160 1165 1170

Asn Lys Lys Glu Ala Val Ile Thr Ile Ala Arg Gly Gln Asn Tyr
1175 1180 1185

Thr Ile Gly Pro Asn Leu Arg Lys Tyr Phe Ser Leu Ser Asn Gly
1190 1195 1200

Ser Asp Leu Pro Asn Arg Asp Phe Thr Ser Ile Ser Ala Ile Gly
1205 1210 1215

Ser Leu Pro Ser Ser Ser Glu Ile Ser Arg Leu Asn Val Gly Asn
1220 1225 1230

Tyr Asn Tyr Arg Val Asn Ala Lys Asn Ala Tyr His Lys Thr Gln
1235 1240 1245

Gln Glu Leu Asn Leu Lys Leu Lys Ile Val Glu Val Asn Ala Pro
1250 1255 1260

Thr Gly Asn Asn Arg Val Tyr Arg Val Ser Thr Tyr Asn Leu Thr
1265 1270 1275

P07741US01_6-19-06_Sequence.txt

Asn Asp Glu Ile Asn Lys Ile Lys Gln Ala Phe Lys Ala Ala Asn
1280 1285 1290

Ser Gly Leu Asn Leu Asn Asp Asn Asp Ile Thr Val Ser Asn Asn
1295 1300 1305

Phe Asp His Arg Asn Val Ser Ser Val Thr Val Thr Ile Arg Lys
1310 1315 1320

Gly Asp Leu Ile Lys Glu Phe Ser Ser Asn Leu Asn Asn Met Asn
1325 1330 1335

Phe Leu Arg Trp Val Asn Ile Arg Asp Asp Tyr Thr Ile Ser Trp
1340 1345 1350

Thr Ser Ser Lys Ile Gln Gly Arg Asn Thr Asp Gly Gly Leu Glu
1355 1360 1365

Trp Ser Pro Asp His Lys Ser Leu Ile Tyr Lys Tyr Asp Ala Thr
1370 1375 1380

Leu Gly Arg Gln Ile Asn Thr Asn Asp Val Leu Thr Leu Leu Gln
1385 1390 1395

Ala Thr Ala Lys Asn Ser Asn Leu Arg Ser Asn Ile Asn Ser Asn
1400 1405 1410

Glu Lys Gln Leu Ala Glu Arg Gly Ser Asn Gly Tyr Ser Lys Ser
1415 1420 1425

Ile Ile Arg Asp Asp Gly Glu Lys Ser Tyr Leu Leu Asn Ser Asn
1430 1435 1440

Pro Ile Gln Val Leu Asp Leu Val Glu Pro Asp Asn Gly Tyr Gly
1445 1450 1455

Gly Arg Gln Val Ser His Ser Asn Val Ile Tyr Asn Glu Lys Asn
1460 1465 1470

P07741US01_6-19-06_Sequence.txt

Ser Ser Ile Val Asn Gly Gln Val Pro Glu Ala Asn Gly Ala Ser
1475 1480 1485

Ala Phe Asn Ile Asp Lys Val Val Lys Ala Asn Ala Ala Asn Asn
1490 1495 1500

Gly Ile Met Gly Val Ile Tyr Lys Ala Gln Leu Tyr Leu Ala Pro
1505 1510 1515

Tyr Ser Pro Lys Gly Tyr Ile Glu Lys Leu Gly Gln Asn Leu Ser
1520 1525 1530

Asn Thr Asn Asn Val Ile Asn Val Tyr Phe Val Pro Ser Asp Lys
1535 1540 1545

Val Asn Pro Ser Ile Thr Val Gly Asn Tyr Asp His His Thr Val
1550 1555 1560

Tyr Ser Gly Glu Thr Phe Lys Asn Thr Ile Asn Val Asn Asp Asn
1565 1570 1575

Tyr Gly Leu Asn Thr Val Ala Ser Thr Ser Asp Ser Ala Ile Thr
1580 1585 1590

Met Thr Arg Asn Asn Asn Glu Leu Val Gly Gln Ala Pro Asn Val
1595 1600 1605

Thr Asn Ser Thr Asn Lys Ile Val Lys Val Lys Ala Thr Asp Lys
1610 1615 1620

Ser Gly Asn Glu Ser Ile Val Ser Phe Thr Val Asn Ile Lys Pro
1625 1630 1635

Leu Asn Glu Lys Tyr Arg Ile Thr Thr Ser Ser Ser Asn Gln Thr
1640 1645 1650

Pro Val Arg Ile Ser Asn Ile Gln Asn Asn Ala Asn Leu Ser Ile
1655 1660 1665

P07741US01_6-19-06_Sequence.txt

Glu Asp Gln Asn Arg Val Lys Ser Ser Leu Ser Met Thr Lys Ile
1670 1675 1680

Leu Gly Thr Arg Asn Tyr Val Asn Glu Ser Asn Asn Asp Val Arg
1685 1690 1695

Ser Gln val Val Ser Lys Val Asn Arg Ser Gly Asn Asn Ala Thr
1700 1705 1710

Val Asn Val Thr Thr Thr Phe Ser Asp Gly Thr Thr Asn Thr Ile
1715 1720 1725

Thr Val Pro Val Lys His Val Leu Leu Glu Val Val Pro Thr Thr
1730 1735 1740

Arg Thr Thr Val Arg Gly Gln Gln Phe Pro Thr Gly Lys Gly Thr
1745 1750 1755

Ser Pro Asn Asp Phe Phe Ser Leu Arg Thr Gly Gly Pro Val Asp
1760 1765 1770

Ala Arg Ile Val Trp Val Asn Asn Gln Gly Pro Asp Ile Asn Ser
1775 1780 1785

Asn Gln Ile Gly Arg Asp Leu Thr Leu His Ala Glu Ile Phe Phe
1790 1795 1800

Asp Gly Glu Thr Thr Pro Ile Arg Lys Asp Thr Thr Tyr Lys Leu
1805 1810 1815

Ser Gln Ser Ile Pro Lys Gln Ile Tyr Glu Thr Thr Ile Asn Gly
1820 1825 1830

Arg Phe Asn Ser Ser Gly Asp Ala Tyr Pro Gly Asn Phe Val Gln
1835 1840 1845

Ala Val Asn Gln Tyr Trp Pro Glu His Met Asp Phe Arg Trp Ala
1850 1855 1860

P07741US01_6-19-06_Sequence.txt

Gln Gly Ser Gly Thr Pro Ser Ser Arg Asn Ala Gly Ser Phe Thr
1865 1870 1875

Lys Thr val Thr val val Tyr Gln Asn Gly Gln Thr Glu Asn Val
1880 1885 1890

Asn Val Leu Phe Lys Val Lys Pro Asn Lys Pro Val Ile Asp Ser
1895 1900 1905

Asn Ser val Ile Ser Lys Gly Gln Leu Asn Gly Gln Gln Ile Leu
1910 1915 1920

val Arg Asn Val Pro Gln Asn Ala Gln Val Thr Leu Tyr Gln Ser
1925 1930 1935

Asn Gly Thr Val Ile Pro Asn Thr Asn Thr Thr Ile Asp Ser Asn
1940 1945 1950

Gly Ile Ala Thr Val Thr Ile Gln Gly Thr Leu Pro Thr Gly Asn
1955 1960 1965

Ile Thr Ala Lys Thr Ser Met Thr Asn Asn Val Thr Tyr Thr Lys
1970 1975 1980

Gln Asn Ser Ser Gly Ile Ala Ser Asn Thr Thr Glu Asp Ile Ser
1985 1990 1995

Val Phe Ser Glu Asn Ser Asp Gln Val Asn Val Thr Ala Gly Met
2000 2005 2010

Gln Ala Lys Asn Asp Gly Ile Lys Ile Ile Lys Gly Thr Asn Tyr
2015 2020 2025

Asn Phe Asn Asp Phe Asn Ser Phe Ile Ser Asn Ile Pro Ala His
2030 2035 2040

Ser Thr Leu Thr Trp Asn Glu Glu Pro Asn Ser Trp Lys Asn Asn
2045 2050 2055

P07741US01_6-19-06_Sequence.txt

Ile Gly Thr Thr Thr Lys Thr Val Thr Val Thr Leu Pro Asn His
2060 2065 2070

Gln Gly Thr Arg Thr Val Asp Ile Pro Ile Thr Ile Tyr Pro Thr
2075 2080 2085

Val Thr Ala Lys Asn Pro Val Arg Asp Gln Lys Gly Arg Asn Leu
2090 2095 2100

Thr Asn Gly Thr Asp Val Tyr Asn Tyr Ile Ile Phe Glu Asn Asn
2105 2110 2115

Asn Arg Leu Gly Gly Thr Ala Ser Trp Lys Asp Asn Arg Gln Pro
2120 2125 2130

Asp Lys Asn Ile Ala Gly Val Gln Asn Leu Ile Ala Leu Val Asn
2135 2140 2145

Tyr Pro Gly Ile Ser Thr Pro Leu Glu Val Pro Val Lys Val Trp
2150 2155 2160

Val Tyr Asn Phe Asp Phe Thr Gln Pro Ile Tyr Lys Ile Gln Val
2165 2170 2175

Gly Asp Thr Phe Pro Lys Gly Thr Trp Ala Gly Tyr Tyr Lys His
2180 2185 2190

Leu Glu Asn Gly Glu Gly Leu Pro Ile Asp Gly Trp Lys Phe Tyr
2195 2200 2205

Trp Asn Gln Gln Ser Thr Gly Thr Thr Ser Asp Gln Trp Gln Ser
2210 2215 2220

Leu Ala Tyr Thr Arg Thr Pro Phe Val Lys Thr Gly Thr Tyr Asp
2225 2230 2235

Val Val Asn Pro Ser Asn Trp Gly Val Trp Gln Thr Ser Gln Ser
2240 2245 2250

P07741US01_6-19-06_Sequence.txt

Ala Lys Phe Ile Val Thr Asn Ala Lys Pro Asn Gln Pro Thr Ile
2255 2260 2265

Thr Gln Ser Lys Thr Gly Asp Val Thr Val Thr Pro Gly Ala Val
2270 2275 2280

Arg Asn Ile Leu Ile Ser Gly Thr Asn Asp Tyr Ile Gln Ala Ser
2285 2290 2295

Ala Asp Lys Ile Val Ile Asn Lys Asn Gly Asn Lys Leu Thr Thr
2300 2305 2310

Phe Val Lys Asn Asn Asp Gly Arg Trp Thr Val Glu Thr Gly Ser
2315 2320 2325

Pro Asp Ile Asn Gly Ile Gly Pro Thr Asn Asn Gly Thr Ala Ile
2330 2335 2340

Ser Leu Ser Arg Leu Ala Val Arg Pro Gly Asp Ser Ile Glu Ala
2345 2350 2355

Ile Ala Thr Glu Gly Ser Gly Glu Thr Ile Ser Thr Ser Ala Thr
2360 2365 2370

Ser Glu Ile Tyr Ile Val Lys Ala Pro Gln Pro Glu Gln Val Ala
2375 2380 2385

Thr His Thr Tyr Asp Asn Gly Thr Phe Asp Ile Leu Pro Asp Asn
2390 2395 2400

Ser Arg Asn Ser Leu Asn Pro Thr Glu Arg Val Glu Ile Asn Tyr
2405 2410 2415

Thr Glu Lys Leu Asn Gly Asn Glu Thr Gln Lys Ser Phe Thr Ile
2420 2425 2430

Thr Lys Asn Asn Asn Gly Lys Trp Thr Ile Asn Asn Lys Pro Asn
2435 2440 2445

P07741US01_6-19-06_Sequence.txt

Tyr Val Glu Phe Asn Gln Asp Asn Gly Lys Val Val Phe Ser Ala
2450 2455 2460

Asn Thr Ile Lys Pro Asn Ser Gln Ile Thr Ile Thr Pro Lys Ala
2465 2470 2475

Gly Gln Gly Asn Thr Glu Asn Thr Asn Pro Thr Val Ile Gln Ala
2480 2485 2490

Pro Ala Gln His Thr Leu Thr Ile Asn Glu Ile Val Lys Glu Gln
2495 2500 2505

Gly Gln Asn Val Thr Asn Asp Asp Ile Asn Asn Ala Val Gln Val
2510 2515 2520

Pro Asn Lys Asn Arg Val Ala Ile Lys Gln Gly Asn Ala Leu Pro
2525 2530 2535

Thr Asn Leu Ala Gly Gly Ser Thr Ser His Ile Pro Val Val Ile
2540 2545 2550

Tyr Tyr Ser Asp Gly Ser Ser Glu Glu Ala Thr Glu Thr Val Arg
2555 2560 2565

Thr Lys Val Asn Lys Thr Glu Leu Ile Asn Ala Arg Arg Arg Leu
2570 2575 2580

Asp Glu Glu Ile Ser Lys Glu Asn Lys Thr Pro Ser Ser Ile Arg
2585 2590 2595

Asn Phe Asp Gln Ala Met Asn Arg Ala Gln Ser Gln Ile Asn Thr
2600 2605 2610

Ala Lys Ser Asp Ala Asp Gln Val Ile Gly Thr Glu Phe Ala Thr
2615 2620 2625

Pro Gln Gln Val Asn Ser Ala Leu Ser Lys Val Gln Ala Ala Gln
2630 2635 2640

P07741US01_6-19-06_Sequence.txt

Asn Lys Ile Asn Glu Ala Lys Ala Leu Leu Gln Asn Lys Ala Asp
2645 2650 2655

Asn Ser Gln Leu Val Arg Ala Lys Glu Gln Leu Gln Gln Ser Ile
2660 2665 2670

Gln Pro Ala Ala Ser Thr Asp Gly Met Thr Gln Asp Ser Thr Arg
2675 2680 2685

Asn Tyr Lys Asn Lys Arg Gln Ala Ala Glu Gln Ala Ile Gln His
2690 2695 2700

Ala Asn Ser Val Ile Asn Asn Gly Asp Ala Thr Ser Gln Gln Ile
2705 2710 2715

Asn Asp Ala Lys Asn Thr val Glu Gln Ala Gln Arg Asp Tyr val
2720 2725 2730

Glu Ala Lys Ser Asn Leu Arg Ala Asp Lys Ser Gln Leu Gln Ser
2735 2740 2745

Ala Tyr Asp Thr Leu Asn Arg Asp Val Leu Thr Asn Asp Lys Lys
2750 2755 2760

Pro Ala Ser Val Arg Arg Tyr Asn Glu Ala Ile Ser Asn Ile Arg
2765 2770 2775

Lys Glu Leu Asp Thr Ala Lys Ala Asp Ala Ser Ser Thr Leu Arg
2780 2785 2790

Asn Thr Asn Pro Ser Val Glu Gln Val Arg Asp Ala Leu Asn Lys
2795 2800 2805

Ile Asn Thr Val Gln Pro Lys Val Asn Gln Ala Ile Ala Leu Leu
2810 2815 2820

Gln Pro Lys Glu Asn Asn Ser Glu Leu Val Gln Ala Lys Lys Arg
2825 2830 2835

P07741US01_6-19-06_Sequence.txt

Leu Gln Asp Ala Val Asn Asp Ile Pro Gln Thr Gln Gly Met Thr
2840 2845 2850

Gln Gln Thr Ile Asn Asn Tyr Asn Asp Lys Gln Arg Glu Ala Glu
2855 2860 2865

Arg Ala Leu Thr Ser Ala Gln Arg Val Ile Asp Asn Gly Asp Ala
2870 2875 2880

Thr Thr Gln Glu Ile Thr Ser Glu Lys Ser Lys Val Glu Gln Ala
2885 2890 2895

Met Gln Ala Leu Thr Asn Ala Lys Ser Asn Leu Arg Ala Asp Lys
2900 2905 2910

Asn Glu Leu Gln Thr Ala Tyr Asn Lys Leu Ile Glu Asn Val Ser
2915 2920 2925

Thr Asn Gly Lys Lys Pro Ala Ser Ile Arg Gln Tyr Glu Thr Ala
2930 2935 2940

Lys Ala Arg Ile Gln Asn Gln Ile Asn Asp Ala Lys Asn Glu Ala
2945 2950 2955

Glu Arg Ile Leu Gly Asn Asp Asn Pro Gln Val Ser Gln Val Thr
2960 2965 2970

Gln Ala Leu Asn Lys Ile Lys Ala Ile Gln Pro Lys Leu Thr Glu
2975 2980 2985

Ala Ile Asn Met Leu Gln Asn Lys Glu Asn Asn Thr Glu Leu Val
2990 2995 3000

Asn Ala Lys Asn Arg Leu Glu Asn Ala Val Asn Asp Thr Asp Pro
3005 3010 3015

Thr His Gly Met Thr Gln Glu Thr Ile Asn Asn Tyr Asn Ala Lys
3020 3025 3030

P07741US01_6-19-06_Sequence.txt

Lys Arg Glu Ala Gln Asn Glu Ile Gln Lys Ala Asn Met Ile Ile
3035 3040 3045

Asn Asn Gly Asp Ala Thr Ala Gln Asp Ile Ser Ser Glu Lys Ser
3050 3055 3060

Lys Val Glu Gln Val Leu Gln Ala Leu Gln Asn Ala Lys Asn Asp
3065 3070 3075

Leu Arg Ala Asp Lys Arg Glu Leu Gln Thr Ala Tyr Asn Lys Leu
3080 3085 3090

Ile Gln Asn Val Asn Thr Asn Gly Lys Lys Pro Ser Ser Ile Gln
3095 3100 3105

Asn Tyr Lys Ser Ala Arg Arg Asn Ile Glu Asn Gln Tyr Asn Thr
3110 3115 3120

Ala Lys Asn Glu Ala His Asn Val Leu Glu Asn Thr Asn Pro Thr
3125 3130 3135

Val Asn Ala Val Glu Asp Ala Leu Arg Lys Ile Asn Ala Ile Gln
3140 3145 3150

Pro Glu Val Thr Lys Ala Ile Asn Ile Leu Gln Asp Lys Glu Asp
3155 3160 3165

Asn Ser Glu Leu Val Arg Ala Lys Glu Lys Leu Asp Gln Ala Ile
3170 3175 3180

Asn Ser Gln Pro Ser Leu Asn Gly Met Thr Gln Glu Ser Ile Asn
3185 3190 3195

Asn Tyr Thr Thr Lys Arg Arg Glu Ala Gln Asn Ile Ala Ser Ser
3200 3205 3210

Ala Asp Thr Ile Ile Asn Asn Gly Asp Ala Ser Ile Glu Gln Ile
3215 3220 3225

P07741US01_6-19-06_Sequence.txt

Thr Glu Asn Lys Ile Arg Val Glu Glu Ala Thr Asn Ala Leu Asn
3230 3235 3240

Glu Ala Lys Gln His Leu Thr Ala Asp Thr Thr Ser Leu Lys Thr
3245 3250 3255

Glu Val Arg Lys Leu Ser Arg Arg Gly Asp Thr Asn Asn Lys Lys
3260 3265 3270

Pro Ser Ser Val Ser Ala Tyr Asn Asn Thr Ile His Ser Leu Gln
3275 3280 3285

Ser Glu Ile Thr Gln Thr Glu Asn Arg Ala Asn Thr Ile Ile Asn
3290 3295 3300

Lys Pro Ile Arg Ser Val Glu Glu Val Asn Asn Ala Leu His Glu
3305 3310 3315

Val Asn Gln Leu Asn Gln Arg Leu Thr Asp Thr Ile Asn Leu Leu
3320 3325 3330

Gln Pro Leu Ala Asn Lys Glu Ser Leu Lys Glu Ala Arg Asn Arg
3335 3340 3345

Leu Glu Ser Lys Ile Asn Glu Thr Val Gln Thr Asp Gly Met Thr
3350 3355 3360

Gln Gln Ser Val Glu Asn Tyr Lys Gln Ala Lys Ile Lys Ala Gln
3365 3370 3375

Asn Glu Ser Ser Ile Ala Gln Thr Leu Ile Asn Asn Gly Asp Ala
3380 3385 3390

Ser Asp Gln Glu Val Ser Thr Glu Ile Glu Lys Leu Asn Gln Lys
3395 3400 3405

Leu Ser Glu Leu Thr Asn Ser Ile Asn His Leu Thr Val Asn Lys
3410 3415 3420

P07741US01_6-19-06_Sequence.txt

Glu Pro Leu Glu Thr Ala Lys Asn Gln Leu Gln Ala Asn Ile Asp
3425 3430 3435

Gln Lys Pro Ser Thr Asp Gly Met Thr Gln Gln Ser Val Gln Ser
3440 3445 3450

Tyr Glu Arg Lys Leu Gln Glu Ala Lys Asp Lys Ile Asn Ser Ile
3455 3460 3465

Asn Asn Val Leu Ala Asn Asn Pro Asp Val Asn Ala Ile Arg Thr
3470 3475 3480

Asn Lys Val Glu Thr Glu Gln Ile Asn Asn Glu Leu Thr Gln Ala
3485 3490 3495

Lys Gln Gly Leu Thr val Asp Lys Gln Pro Leu Ile Asn Ala Lys
3500 3505 3510

Thr Ala Leu Gln Gln Ser Leu Asp Asn Gln Pro Ser Thr Thr Gly
3515 3520 3525

Met Thr Glu Ala Thr Ile Gln Asn Tyr Asn Ala Lys Arg Gln Lys
3530 3535 3540

Ala Glu Gln Val Ile Gln Asn Ala Asn Lys Ile Ile Glu Asn Ala
3545 3550 3555

Gln Pro Ser Val Gln Gln Val Ser Asp Glu Lys Ser Lys Val Glu
3560 3565 3570

Gln Ala Leu Ser Glu Leu Asn Asn Ala Lys Ser Ala Leu Arg Ala
3575 3580 3585

Asp Lys Gln Glu Leu Gln Gln Ala Tyr Asn Gln Leu Ile Gln Pro
3590 3595 3600

Thr Asp Leu Asn Asn Lys Lys Pro Ala Ser Ile Thr Ala Tyr Asn
3605 3610 3615

P07741US01_6-19-06_Sequence.txt

Gln Arg Tyr Gln Gln Phe Ser Asn Glu Leu Asn Ser Thr Lys Thr
3620 3625 3630

Asn Thr Asp Arg Ile Leu Lys Glu Gln Asn Pro Ser Val Ala Asp
3635 3640 3645

Val Asn Asn Ala Leu Asn Lys Val Arg Glu Val Gln Gln Lys Leu
3650 3655 3660

Asn Glu Ala Arg Ala Leu Leu Gln Asn Lys Glu Asp Asn Ser Ala
3665 3670 3675

Leu Val Arg Ala Lys Glu Gln Leu Gln Gln Ala Val Asp Gln Val
3680 3685 3690

Pro Ser Thr Glu Gly Met Thr Gln Gln Thr Lys Asp Asp Tyr Asn
3695 3700 3705

Ser Lys Gln Gln Ala Ala Gln Gln Glu Ile Ser Lys Ala Gln Gln
3710 3715 3720

Val Ile Asp Asn Gly Asp Ala Thr Thr Gln Gln Ile Ser Asn Ala
3725 3730 3735

Lys Thr Asn Val Glu Arg Ala Leu Glu Ala Leu Asn Asn Ala Lys
3740 3745 3750

Thr Gly Leu Arg Ala Asp Lys Glu Glu Leu Gln Asn Ala Tyr Asn
3755 3760 3765

Gln Leu Thr Gln Asn Ile Asp Thr Ser Gly Lys Thr Pro Ala Ser
3770 3775 3780

Ile Arg Lys Tyr Asn Glu Ala Lys Ser Arg Ile Gln Thr Gln Ile
3785 3790 3795

Asp Ser Ala Lys Asn Glu Ala Asn Ser Ile Leu Thr Asn Asp Asn
3800 3805 3810

P07741US01_6-19-06_Sequence.txt

Pro Gln Val Ser Gln Val Thr Ala Ala Leu Asn Lys Ile Lys Ala
3815 3820 3825

Val Gln Pro Glu Leu Asp Lys Ala Ile Ala Met Leu Lys Asn Lys
3830 3835 3840

Glu Asn Asn Asn Ala Leu Val Gln Ala Lys Gln Gln Leu Gln Gln
3845 3850 3855

Ile Val Asn Glu Val Asp Pro Thr Gln Gly Met Thr Thr Asp Thr
3860 3865 3870

Ala Asn Asn Tyr Lys Ser Lys Lys Arg Glu Ala Glu Asp Glu Ile
3875 3880 3885

Gln Lys Ala Gln Gln Ile Ile Asn Asn Gly Asp Ala Thr Glu Gln
3890 3895 3900

Gln Ile Thr Asn Glu Thr Asn Arg Val Asn Gln Ala Ile Asn Ala
3905 3910 3915

Ile Asn Lys Ala Lys Asn Asp Leu Arg Ala Asp Lys Ser Gln Leu
3920 3925 3930

Glu Asn Ala Tyr Asn Gln Leu Ile Gln Asn Val Asp Thr Asn Gly
3935 3940 3945

Lys Lys Pro Ala Ser Ile Gln Gln Tyr Gln Ala Ala Arg Gln Ala
3950 3955 3960

Ile Glu Thr Gln Tyr Asn Asn Ala Lys Ser Glu Ala His Gln Ile
3965 3970 3975

Leu Glu Asn Ser Asn Pro Ser Val Asn Glu Val Ala Gln Ala Leu
3980 3985 3990

Gln Lys Val Glu Ala Val Gln Leu Lys Val Asn Asp Ala Ile His
3995 4000 4005

P07741US01_6-19-06_Sequence.txt

Ile Leu Gln Asn Lys Glu Asn Asn Ser Ala Leu Val Thr Ala Lys
4010 4015 4020

Asn Gln Leu Gln Gln Ser Val Asn Asp Gln Pro Leu Thr Thr Gly
4025 4030 4035

Met Thr Gln Asp Ser Ile Asn Asn Tyr Glu Ala Lys Arg Asn Glu
4040 4045 4050

Ala Gln Ser Ala Ile Arg Asn Ala Glu Ala Val Ile Asn Asn Gly
4055 4060 4065

Asp Ala Thr Ala Lys Gln Ile Ser Asp Glu Lys Ser Lys Val Glu
4070 4075 4080

Gln Ala Leu Ala His Leu Asn Asp Ala Lys Gln Gln Leu Thr Ala
4085 4090 4095

Asp Thr Thr Glu Leu Gln Thr Ala Val Gln Gln Leu Asn Arg Arg
4100 4105 4110

Gly Asp Thr Asn Asn Lys Lys Pro Arg Ser Ile Asn Ala Tyr Asn
4115 4120 4125

Lys Ala Ile Gln Ser Leu Glu Thr Gln Ile Thr Ser Ala Lys Asp
4130 4135 4140

Asn Ala Asn Ala Val Ile Gln Lys Pro Ile Arg Thr Val Gln Glu
4145 4150 4155

Val Asn Asn Ala Leu Gln Gln Val Asn Gln Leu Asn Gln Gln Leu
4160 4165 4170

Thr Glu Ala Ile Asn Gln Leu Gln Pro Leu Ser Asn Asn Asp Ala
4175 4180 4185

Leu Lys Ala Ala Arg Leu Asn Leu Glu Asn Lys Ile Asn Gln Thr
4190 4195 4200

P07741US01_6-19-06_Sequence.txt

Val Gln Thr Asp Gly Met Thr Gln Gln Ser Ile Glu Ala Tyr Gln
4205 4210 4215

Asn Ala Lys Arg Val Ala Gln Asn Glu Ser Asn Thr Ala Leu Ala
4220 4225 4230

Leu Ile Asn Asn Gly Asp Ala Asp Glu Gln Gln Ile Thr Thr Glu
4235 4240 4245

Thr Asp Arg Val Asn Gln Gln Thr Thr Asn Leu Thr Gln Ala Ile
4250 4255 4260

Asn Gly Leu Thr Val Asn Lys Glu Pro Leu Glu Thr Ala Lys Thr
4265 4270 4275

Ala Leu Gln Asn Asn Ile Asp Gln Val Pro Ser Thr Asp Gly Met
4280 4285 4290

Thr Gln Gln Ser Val Ala Asn Tyr Asn Gln Lys Leu Gln Ile Ala
4295 4300 4305

Lys Asn Glu Ile Asn Thr Ile Asn Asn Val Leu Ala Asn Asn Pro
4310 4315 4320

Asp Val Asn Ala Ile Lys Thr Asn Lys Ala Glu Ala Glu Arg Ile
4325 4330 4335

Ser Asn Asp Leu Thr Gln Ala Lys Asn Asn Leu Gln Val Asp Thr
4340 4345 4350

Gln Pro Leu Glu Lys Ile Lys Arg Gln Leu Gln Asp Glu Ile Asp
4355 4360 4365

Gln Gly Thr Asn Thr Asp Gly Met Thr Gln Asp Ser Val Asp Asn
4370 4375 4380

Tyr Asn Asp Ser Leu Ser Ala Ala Ile Ile Glu Lys Gly Lys Val
4385 4390 4395

P07741US01_6-19-06_Sequence.txt

Asn Lys Leu Leu Lys Arg Asn Pro Thr Val Glu Gln Val Lys Glu
4400 4405 4410

Ser Val Ala Asn Ala Gln Gln Val Ile Gln Asp Leu Gln Asn Ala
4415 4420 4425

Arg Thr Ser Leu Val Pro Asp Lys Thr Gln Leu Gln Glu Ala Lys
4430 4435 4440

Asn Arg Leu Glu Asn Ser Ile Asn Gln Gln Thr Asp Thr Asp Gly
4445 4450 4455

Met Thr Gln Asp Ser Leu Asn Asn Tyr Asn Asp Lys Leu Ala Lys
4460 4465 4470

Ala Arg Gln Asn Leu Glu Lys Ile Ser Lys Val Leu Gly Gly Gln
4475 4480 4485

Pro Thr Val Ala Glu Ile Arg Gln Asn Thr Asp Glu Ala Asn Ala
4490 4495 4500

His Lys Gln Ala Leu Asp Thr Ala Arg Ser Gln Leu Thr Leu Asn
4505 4510 4515

Arg Glu Pro Tyr Ile Asn His Ile Asn Asn Glu Ser His Leu Asn
4520 4525 4530

Asn Ala Gln Lys Asp Asn Phe Lys Ala Gln Val Asn Ser Ala Pro
4535 4540 4545

Asn His Asn Thr Leu Glu Thr Ile Lys Asn Lys Ala Asp Thr Leu
4550 4555 4560

Asn Gln Ser Met Thr Ala Leu Ser Glu Ser Ile Ala Asp Tyr Glu
4565 4570 4575

Asn Gln Lys Gln Gln Glu Asn Tyr Leu Asp Ala Ser Asn Asn Lys
4580 4585 4590

P07741US01_6-19-06_Sequence.txt

Arg Gln Asp Tyr Asp Asn Ala Val Asn Ala Ala Lys Gly Ile Leu
4595 4600 4605

Asn Gln Thr Gln Ser Pro Thr Met Ser Ala Asp Val Ile Asp Gln
4610 4615 4620

Lys Ala Glu Asp Val Lys Arg Thr Lys Thr Ala Leu Asp Gly Asn
4625 4630 4635

Gln Arg Leu Glu Val Ala Lys Gln Gln Ala Leu Asn His Leu Asn
4640 4645 4650

Thr Leu Asn Asp Leu Asn Asp Ala Gln Arg Gln Thr Leu Thr Asp
4655 4660 4665

Thr Ile Asn His Ser Pro Asn Ile Asn Ser Val /Asn Gln Ala Lys
4670 4675 4680

Glu Lys Ala Asn Thr Val Asn Thr Ala Met Thr Gln Leu Lys Gln
4685 4690 4695

Thr Ile Ala Asn Tyr Asp Asp Glu Leu His Asp Gly Asn Tyr Ile
4700 4705 4710

Asn Ala Asp Lys Asp Lys Lys Asp Ala Tyr Asn Asn Ala Val Asn
4715 4720 4725

Asn Ala Lys Gln Leu Ile Asn Gln Ser Asp Ala Asn Gln Ala Gln
4730 4735 4740

Leu Asp Pro Ala Glu Ile Asn Lys Val Thr Gln Arg Val Asn Thr
4745 4750 4755

Thr Lys Asn Asp Leu Asn Gly Asn Asp Lys Leu Ala Glu Ala Lys
4760 4765 4770

Arg Asp Ala Asn Thr Thr Ile Asp Gly Leu Thr Tyr Leu Asn Glu
4775 4780 4785

P07741US01_6-19-06_Sequence.txt

Ala Gln Arg Asn Lys Ala Lys Glu Asn Val Gly Lys Ala Ser Thr
4790 4795 4800

Lys Thr Asn Ile Thr Ser Gln Leu Gln Asp Tyr Asn Gln Leu Asn
4805 4810 4815

Ile Ala Met Gln Ala Leu Arg Asn Ser Val Asn Asp Val Asn Asn
4820 4825 4830

Val Lys Ala Asn Ser Asn Tyr Ile Asn Glu Asp Asn Gly Pro Lys
4835 4840 4845

Glu Ala Tyr Asn Gln Ala Val Thr His Ala Gln Thr Leu Ile Asn
4850 4855 4860

Ala Gln Ser Asn Pro Glu Met Ser Arg Asp Val Val Asn Gln Lys
4865 4870 4875

Thr Gln Ala Val Asn Thr Ala His Gln Asn Leu His Gly Gln Gln
4880 4885 4890

Lys Leu Glu Gln Ala Gln Ser Ser Ala Asn Thr Glu Ile Gly Asn
4895 4900 4905

Leu Pro Asn Leu Thr Asn Thr Gln Lys Ala Lys Glu Lys Glu Leu
4910 4915 4920

Val Asn Ser Lys Gln Thr Arg Thr Glu Val Gln Glu Gln Leu Asn
4925 4930 4935

Gln Ala Lys Ser Leu Asp Ser Ser Met Gly Thr Leu Lys Ser Leu
4940 4945 4950

Val Ala Lys Gln Pro Thr Val Gln Lys Thr Ser Val Tyr Ile Asn
4955 4960 4965

Glu Asp Gln Pro Glu Gln Ser Ala Tyr Asn Asp Ser Ile Thr Met
4970 4975 4980

P07741US01_6-19-06_Sequence.txt

Gly Gln Thr Ile Ile Asn Lys Thr Ala Asp Pro Val Leu Asp Lys
4985 4990 4995

Thr Leu Val Asp Asn Ala Ile Ser Asn Ile Ser Thr Lys Glu Asn
5000 5005 5010

Ala Leu His Gly Glu Gln Lys Leu Thr Thr Ala Lys Thr Glu Ala
5015 5020 5025

Ile Asn Ala Leu Asn Thr Leu Ala Asp Leu Asn Thr Pro Gln Lys
5030 5035 5040

Glu Ala Ile Lys Thr Ala Ile Asn Thr Ala His Thr Arg Thr Asp
5045 5050 5055

Val Thr Ala Glu Gln Ser Lys Ala Asn Gln Ile Asn Ser Ala Met
5060 5065 5070

His Thr Leu Arg Gln Asn Ile Ser Asp Asn Glu Ser Val Thr Asn
5075 5080 5085

Glu Ser Asn Tyr Ile Asn Ala Glu Pro Glu Lys Gln His Ala Phe
5090 5095 5100

Thr Glu Ala Leu Asn Asn Ala Lys Glu Ile Val Asn Glu Gln Gln
5105 5110 5115

Ala Thr Leu Asp Ala Asn Ser Ile Asn Gln Lys Ala Gln Ala Ile
5120 5125 5130

Leu Thr Thr Lys Asn Ala Leu Asp Gly Glu Glu Gln Leu Arg Arg
5135 5140 5145

Ala Lys Glu Asn Ala Asp Gln Glu Ile Asn Thr Leu Asn Gln Leu
5150 5155 5160

Thr Asp Ala Gln Arg Asn Ser Glu Lys Gly Leu Val Asn Ser Ser
5165 5170 5175

P07741US01_6-19-06_Sequence.txt

Gln Thr Arg Thr Glu Val Ala Ser Gln Leu Ala Lys Ala Lys Glu
5180 5185 5190

Leu Asn Lys Val Met Glu Gln Leu Asn His Leu Ile Asn Gly Lys
5195 5200 5205

Asn Gln Met Ile Asn Ser Ser Lys Phe Ile Asn Glu Asp Ala Asn
5210 5215 5220

Gln Gln Gln Ala Tyr Ser Asn Ala Ile Ala Ser Ala Glu Ala Leu
5225 5230 5235

Lys Asn Lys Ser Gln Asn Pro Glu Leu Asp Lys Val Thr Ile Glu
5240 5245 5250

Gln Ala Ile Asn Asn Ile Asn Ser Ala Ile Asn Asn Leu Asn Gly
5255 5260 5265

Glu Ala Lys Leu Thr Lys Ala Lys Glu Asp Ala Val Ala Ser Ile
5270 5275 5280

Asn Asn Leu Ser Gly Leu Thr Asn Glu Gln Lys Pro Lys Glu Asn
5285 5290 5295

Gln Ala Val Asn Gly Ala Gln Thr Arg Asp Gln Val Ala Asn Lys
5300 5305 5310

Leu Arg Asp Ala Glu Ala Leu Asp Gln Ser Met Gln Thr Leu Arg
5315 5320 5325

Asp Leu Val Asn Asn Gln Asn Ala Ile His Ser Thr Ser Asn Tyr
5330 5335 5340

Phe Asn Glu Asp Ser Thr Gln Lys Asn Thr Tyr Asp Asn Ala Ile
5345 5350 5355

Asp Asn Gly Ser Thr Tyr Ile Thr Gly Gln His Asn Pro Glu Leu
5360 5365 5370

P07741US01_6-19-06_Sequence.txt

Asn Lys Ser Thr Ile Asp Gln Thr Ile Ser Arg Ile Asn Thr Ala
5375 5380 5385

Lys Asn Asp Leu His Gly Val Glu Lys Leu Gln Arg Asp Lys Gly
5390 5395 5400

Thr Ala Asn Gln Glu Ile Gly Gln Leu Gly Tyr Leu Asn Asp Pro .
5405 5410 5415

Gln Lys Ser Gly Glu Glu Ser Leu Val Asn Gly Ser Asn Thr Arg
5420 5425 5430

Ser Glu Val Glu Glu His Leu Asn Glu Ala Lys Ser Leu Asn Asn
5435 5440 5445

Ala Met Lys Gln Leu Arg Asp Lys Val Ala Glu Lys Thr Asn Val
5450 5455 5460

Lys Gln Ser Ser Asp Tyr Ile Asn Asp Ser Thr Glu His Gln Arg
5465 5470 5475

Gly Tyr Asp Gln Ala Leu Gln Glu Ala Glu Asn Ile Ile Asn Glu
5480 5485 5490

Ile Gly Asn Pro Thr Leu Asn Lys Ser Glu Ile Glu Gln Lys Leu
5495 5500 5505

Gln Gln Leu Thr Asp Ala Gln Asn Ala Leu Gln Gly Ser His Leu
5510 5515 5520

Leu Glu Glu Ala Lys Asn Asn Ala Ile Thr Gly Ile Asn Lys Leu
5525 5530 5535

Thr Ala Leu Asn Asp Ala Gln Arg Gln Lys Ala Ile Glu Asn Val
5540 5545 5550

Gln Ala Gln Gln Thr Ile Pro Ala Val Asn Gln Gln Leu Thr Leu
5555 5560 5565

P07741US01_6-19-06_Sequence.txt

Asp Arg Glu Ile Asn Thr Ala Met Gln Ala Leu Arg Asp Lys Val
5570 5575 5580

Gly Gln Gln Asn Asn Val His Gln Gln Ser Asn Tyr Phe Asn Glu
5585 5590 5595

Asp Glu Gln Pro Lys His Asn Tyr Asp Asn Ser Val Gln Ala Gly
5600 5605 5610

Gln Thr Ile Ile Asp Lys Leu Gln Asp Pro Ile Met Asn Lys Asn
5615 5620 5625

Glu Ile Glu Gln Ala Ile Asn Gln Ile Asn Thr Thr Gln Thr Ala
5630 5635 5640

Leu Ser Gly Glu Asn Lys Leu His Thr Asp Gln Glu Ser Thr Asn
5645 5650 5655

Arg Gln Ile Glu Gly Leu Ser Ser Leu Asn Thr Ala Gln Ile Asn
5660 5665 5670

Ala Glu Lys Asp Leu Val Asn Gln Ala Lys Thr Arg Thr Asp Val
5675 5680 5685

Ala Gln Lys Leu Ala Ala Ala Lys Glu Ile Asn Ser Ala Met Ser
5690 5695 5700

Asn Leu Arg Asp Gly Ile Gln Asn Lys Glu Asp Ile Lys Arg Ser
5705 5710 5715

Ser Ala Tyr Ile Asn Ala Asp Pro Thr Lys Val Thr Ala Tyr Asp
5720 5725 5730

Gln Ala Leu Gln Asn Ala Glu Asn Ile Ile Asn Ala Thr Pro Asn
5735 5740 5745

Val Glu Leu Asn Lys Ala Thr Ile Glu Gln Ala Leu Ser Arg Val
5750 5755 5760

P07741US01_6-19-06_Sequence.txt

Gln Gln Ala Gln Gln Asp Leu Asp Gly Val Gln Gln Leu Ala Asn
5765 5770 5775

Ala Lys Gln Gln Ala Thr Gln Thr Val Asn Gly Leu Asn Ser Leu
5780 5785 5790

Asn Asp Gly Gln Lys Arg Glu Leu Asn Leu Leu Ile Asn Ser Ala
5795 5800 5805

Asn Thr Arg Thr Lys Val Gln Glu Glu Leu Asn Lys Ala Thr Glu
5810 5815 5820

Leu Asn His Ala Met Glu Ala Leu Arg Asn Ser Val Gln Asn Val
5825 5830 5835

Asp Gln Val Lys Gln Ser Ser Asn Tyr Val Asn Glu Asp Gln Pro
5840 5845 5850

Glu Gln His Asn Tyr Asp Asn Ala Val Asn Glu Ala Gln Ala Thr
5855 5860 5865

Ile Asn Asn Asn Ala Gln Pro Val Leu Asp Lys Leu Ala Ile Glu
5870 5875 5880

Arg Leu Thr Gln Thr Val Asn Thr Thr Lys Asp Ala Leu His Gly
5885 5890 5895

Ala Gln Lys Leu Thr Gln Asp Gln Gln Ala Ala Glu Thr Gly Ile
5900 5905 5910

Arg Gly Leu Thr Ser Leu Asn Glu Pro Gln Lys Asn Ala Glu Val
5915 5920 5925

Ala Lys Val Thr Ala Ala Thr Thr Arg Asp Glu Val Arg Asn Ile
5930 5935 5940

Arg Gln Glu Ala Thr Thr Leu Asp Thr Ala Met Leu Gly Leu Arg
5945 5950 5955

P07741US01_6-19-06_Sequence.txt

Lys Ser Ile Lys Asp Lys Asn Asp Thr Lys Asn Ser Ser Lys Tyr
5960 5965 5970

Ile Asn Glu Asp His Asp Gln Gln Gln Ala Tyr Asp Asn Ala Val
5975 5980 5985

Asn Asn Ala Gln Gln Val Ile Asp Glu Thr Gln Ala Thr Leu Ser
5990 5995 6000

Ser Asp Thr Ile Asn Gln Leu Ala Asn Ala Val Thr Gln Ala Lys
6005 6010 6015

Ser Asn Leu His Gly Asp Thr Lys Leu Gln His Asp Lys Asp Ser
6020 6025 6030

Ala Lys Gln Thr Ile Ala Gln Leu Gln Asn Leu Asn Ser Ala Gln
6035 6040 6045

Lys His Met Glu Asp Ser Leu Ile Asp Asn Glu Ser Thr Arg Thr
6050 6055 6060

Gln Val Gln His Asp Leu Thr Glu Ala Gln Ala Leu Asp Gly Leu
6065 6070 6075

Met Gly Ala Leu Lys Glu Ser Ile Lys Asp Tyr Thr Asn Ile Val
6080 6085 6090

Ser Asn Gly Asn Tyr Ile Asn Ala Glu Pro Ser Lys Lys Gln Ala
6095 6100 6105

Tyr Asp Ala Ala Val Gln Asn Ala Gln Asn Ile Ile Asn Gly Thr
6110 6115 6120

Asn Gln Pro Thr Ile Asn Lys Gly Asn Val Thr Thr Ala Thr Gln
6125 6130 6135

Thr Val Lys Asn Thr Lys Asp Ala Leu Asp Gly Asp His Arg Leu
6140 6145 6150

P07741US01_6-19-06_Sequence.txt

Glu Glu Ala Lys Asn Asn Ala Asn Gln Thr Ile Arg Asn Leu Ser
6155 6160 6165

Asn Leu Asn Asn Ala Gln Lys Asp Ala Glu Lys Asn Leu Val Asn
6170 6175 6180

Ser Ala Ser Thr Leu Glu Gln Val Gln Gln Asn Leu Gln Thr Ala
6185 6190 6195

Gln Gln Leu Asp Asn Ala Met Gly Glu Leu Arg Gln Ser Ile Ala
6200 6205 6210

Lys Lys Asp Gln Val Lys Ala Asp Ser Lys Tyr Leu Asn Glu Asp
6215 6220 6225

Pro Gln Ile Lys Gln Asn Tyr Asp Asp Ala val Gln Arg Val Glu
6230 6235 6240

Thr Ile Ile Asn Glu Thr Gln Asn Pro Glu Leu Leu Lys Ala Asn
6245 6250 6255

Ile Asp Gln Ala Thr Gln Ser Val Gln Asn Ala Glu Gln Ala Leu
6260 6265 6270

His Gly Ala Glu Lys Leu Asn Gln Asp Lys Gln Thr Ser Ser Thr
6275 6280 6285

Glu Leu Asp Gly Leu Thr Asp Leu Thr Asp Ala Gln Arg Glu Lys
6290 6295 6300

Leu Arg Glu Gln Ile Asn Thr Ser Asn Ser Arg Asp Asp Ile Lys
6305 6310 6315

Gln Lys Ile Glu Gln Ala Lys Ala Leu Asn Asp Ala Met Lys Lys
6320 6325 6330

Leu Lys Glu Gln Val Ala Gln Lys Asp Gly Val His Ala Asn Ser
6335 6340 6345

P07741US01_6-19-06_Sequence.txt

Asp Tyr Thr Asn Glu Asp Ser Ala Gln Lys Asp Ala Tyr Asn Asn
6350 6355 6360

Ala Leu Lys Gln Ala Glu Asp Ile Ile Asn Asn Ser Ser Asn Pro
6365 6370 6375

Asn Leu Asn Ala Gln Asp Ile Thr Asn Ala Leu Asn Asn Ile Lys
6380 6385 6390

Gln Ala Gln Asp Asn Leu His Gly Ala Gln Lys Leu Gln Gln Asp
6395 6400 6405

Lys Asn Thr Thr Asn Gln Ala Ile Gly Asn Leu Asn His Leu Asn
6410 6415 6420

Gln Pro Gln Lys Asp Ala Leu Ile Gln Ala Ile Asn Gly Ala Thr
6425 6430 6435

Ser Arg Asp Gln Val Ala Glu Lys Leu Lys Glu Ala Glu Ala Leu
6440 6445 6450

Asp Glu Ala Met Lys Gln Leu Glu Asp Gln Val Asn Gln Asp Asp
6455 6460 6465

Gln Ile Ser Asn Ser Ser Pro Phe Ile Asn Glu Asp Ser Asp Lys
6470 6475 6480

Gln Lys Thr Tyr Asn Asp Lys Ile Gln Ala Ala Lys Glu Ile Ile
6485 6490 6495

Asn Gln Thr Ser Asn Pro Thr Leu Asp Lys Gln Lys Ile Ala Asp
6500 6505 6510

Thr Leu Gln Asn Ile Lys Asp Ala Val Asn Asn Leu His Gly Asp
6515 6520 6525

Gln Lys Leu Ala Gln Ser Lys Gln Asp Ala Asn Asn Gln Leu Asn
6530 6535 6540

P07741US01_6-19-06_Sequence.txt

His Leu Asp Asp Leu Thr Glu Glu Gln Lys Asn His Phe Lys Pro
6545 6550 6555

Leu Ile Asn Asn Ala Asp Thr Arg Asp Glu Val Asn Lys Gln Leu
6560 6565 6570

Glu Ile Ala Lys Gln Leu Asn Gly Asp Met Ser Thr Leu His Lys
6575 6580 6585

Val Ile Asn Asp Lys Asp Gln Ile Gln His Leu Ser Asn Tyr Ile
6590 6595 6600

Asn Ala Asp Asn Asp Lys Lys Gln Asn Tyr Asp Asn Ala Ile Lys
6605 6610 6615

Glu Ala Glu Asp Leu Ile His Asn His Pro Asp Thr Leu Asp His
6620 6625 6630

Lys Ala Leu Gln Asp Leu Leu Asn Lys Ile Asp Gln Ala His Asn
6635 6640 6645

Glu Leu Asn Gly Glu Ser Arg Phe Lys Gln Ala Leu Asp Asn Ala
6650 6655 6660

Leu Asn Asp Ile Asp Ser Leu Asn Ser Leu Asn Val Pro Gln Arg
6665 6670 6675

Gln Thr Val Lys Asp Asn Ile Asn His Val Thr Thr Leu Glu Ser
6680 6685 6690

Leu Ala Gln Glu Leu Gln Lys Ala Lys Glu Leu Asn Asp Ala Met
6695 6700 6705

Lys Ala Met Arg Asp Ser Ile Met Asn Gln Glu Gln Ile Arg Lys
6710 6715 6720

Asn Ser Asn Tyr Thr Asn Glu Asp Leu Ala Gln Gln Asn Ala Tyr
6725 6730 6735

P07741US01_6-19-06_Sequence.txt

Asn His Ala Val Asp Lys Ile Asn Asn Ile Ile Gly Glu Asp Asn
6740 6745 6750

Ala Thr Met Asp Pro Gln Ile Ile Lys Gln Ala Thr Gln Asp Ile
6755 6760 6765

Asn Thr Ala Ile Asn Gly Leu Asn Gly Asp Gln Lys Leu Gln Asp
6770 6775 6780

Ala Lys Thr Asp Ala Lys Gln Gln Ile Thr Asn Phe Thr Gly Leu
6785 6790 6795

Thr Glu Pro Gln Lys Gln Ala Leu Glu Asn Ile Ile Asn Gln Gln
6800 6805 6810

Thr Ser Arg Ala Asn Val Ala Lys Gln Leu Ser His Ala Lys Phe
6815 6820 6825

Leu Asn Gly Lys Met Glu Glu Leu Lys Val Ala Val Ala Lys Ala
6830 6835 6840

Ser Leu Val Arg Gln Asn Ser Asn Tyr Ile Asn Glu Asp Val Ser
6845 6850 6855

Glu Lys Glu Ala Tyr Glu Gln Ala Ile Ala Lys Gly Gln Glu Ile
6860 6865 6870

Ile Asn Ser Glu Asn Asn Pro Thr Ile Ser Ser Thr Asp Ile Asn
6875 6880 6885

Arg Thr Ile Gln Glu Ile Asn Asp Ala Glu Gln Asn Leu His Gly
6890 6895 6900

Asp Asn Lys Leu Arg Gln Ala Gln Glu Ile Ala Lys Asn Glu Ile
6905 6910 6915

Gln Asn Leu Asp Gly Leu Asn Ser Ala Gln Ile Thr Lys Leu Ile
6920 6925 6930

P07741US01_6-19-06_Sequence.txt

Gln Asp Ile Gly Arg Thr Thr Thr Lys Pro Ala Val Thr Gln Lys
6935 6940 6945

Leu Glu Glu Ala Lys Ala Ile Asn Gln Ala Met Gln Gln Leu Lys
6950 6955 6960

Gln Ser Ile Ala Asp Lys Asp Ala Thr Leu Asn Ser Ser Asn Tyr
6965 6970 6975

Leu Asn Glu Asp Ser Glu Lys Lys Leu Ala Tyr Asp Asn Ala Val
6980 6985 6990

Ser Gln Ala Glu Gln Leu Ile Asn Gln Leu Asn Asp Pro Thr Met
6995 7000 7005

Asp Ile Ser Asn Ile Gln Ala Ile Thr Gln Lys Val Ile Gln Ala
7010 7015 7020

Lys Asp Ser Leu His Gly Ala Asn Lys Leu Ala Gln Asn Gln Ala
7025 7030 7035

Asp Ser Asn Leu Ile Ile Asn Gln Ser Thr Asn Leu Asn Asp Lys
7040 7045 7050

Gln Lys Gln Ala Leu Asn Asp Leu Ile Asn His Ala Gln Thr Lys
7055 7060 7065

Gln Gln Val Ala Glu Ile Ile Ala Gln Ala Asn Lys Leu Asn Asn
7070 7075 7080

Glu Met Gly Thr Leu Lys Thr Leu Val Glu Glu Gln Ser Asn Val
7085 7090 7095

His Gln Gln Ser Lys Tyr Ile Asn Glu Asp Pro Gln Val Gln Asn
7100 7105 7110

Ile Tyr Asn Asp Ser Ile Gln Lys Gly Arg Glu Ile Leu Asn Gly
7115 7120 7125

P07741US01_6-19-06_Sequence.txt

Thr Thr Asp Asp Val Leu Asn Asn Asn Lys Ile Ala Asp Ala Ile
7130 7135 7140

Gln Asn Ile His Leu Thr Lys Asn Asp Leu His Gly Asp Gln Lys
7145 7150 7155

Leu Gln Lys Ala Gln Gln Asp Ala Thr Asn Glu Leu Asn Tyr Leu
7160 7165 7170

Thr Asn Leu Asn Asn Ser Gln Arg Gln Ser Glu His Asp Glu Ile
7175 7180 7185

Asn Ser Ala Pro Ser Arg Thr Glu Val Ser Asn Asp Leu Asn His
7190 7195 7200

Ala Lys Ala Leu Asn Glu Ala Met Arg Gln Leu Glu Asn Glu Val
7205 7210 7215

Ala Leu Glu Asn Ser Val Lys Lys Leu Ser Asp Phe Ile Asn Glu
7220 7225 7230

Asp Glu Ala Ala Gln Asn Glu Tyr Ser Asn Ala Leu Gln Lys Ala
7235 7240 7245

Lys Asp Ile Ile Asn Gly Val Pro Ser Ser Thr Leu Asp Lys Ala
7250 7255 7260

Thr Ile Glu Asp Ala Leu Leu Glu Leu Gln Asn Ala Arg Glu Ser
7265 7270 7275

Leu His Gly Glu Gln Lys Leu Gln Glu Ala Lys Asn Gln Ala Val
7280 7285 7290

Ala Glu Ile Asp Asn Leu Gln Ala Leu Asn Pro Gly Gln Val Leu
7295 7300 7305

Ala Glu Lys Thr Leu Val Asn Gln Ala Ser Thr Lys Pro Glu Val
7310 7315 7320

P07741US01_6-19-06_Sequence.txt

Gln Glu Ala Leu Gln Lys Ala Lys Glu Leu Asn Glu Ala Met Lys
7325 7330 7335

Ala Leu Lys Thr Glu Ile Asn Lys Lys Glu Gln Ile Lys Ala Asp
7340 7345 7350

Ser Arg Tyr Val Asn Ala Asp Ser Gly Leu Gln Ala Asn Tyr Asn
7355 7360 7365

Ser Ala Leu Asn Tyr Gly Ser Gln Ile Ile Ala Thr Thr Gln Pro
7370 7375 7380

Pro Glu Leu Asn Lys Asp Val Ile Asn Arg Ala Thr Gln Thr Ile
7385 7390 7395

Lys Thr Ala Glu Asn Asn Leu Asn Gly Gln Ser Lys Leu Ala Glu
7400 7405 7410

Ala Lys Ser Asp Gly Asn Gln Ser Ile Glu His Leu Gln Gly Leu
7415 7420 7425

Thr Gln Ser Gln Lys Asp Lys Gln His Asp Leu Ile Asn Gln Ala
7430 7435 7440

Gln Thr Lys Gln Gln Val Asp Asp Ile Val Asn Asn Ser Lys Gln
7445 7450 7455

Leu Asp Asn Ser Met Asn Gln Leu Gln Gln Ile Val Asn Asn Asp
7460 7465 7470

Asn Thr Val Lys Gln Asn Ser Asp Phe Ile Asn Glu Asp Ser Ser
7475 7480 7485

Gln Gln Asp Ala Tyr Asn His Ala Ile Gln Ala Ala Lys Asp Leu
7490 7495 7500

Ile Thr Ala His Pro Thr Ile Met Asp Lys Asn Gln Ile Asp Gln
7505 7510 7515

P07741US01_6-19-06_Sequence.txt

Ala Ile Glu Asn Ile Lys Gln Ala Leu Asn Asp Leu His Gly Ser
7520 7525 7530

Asn Lys Leu Ser Glu Asp Lys Lys Glu Ala Ser Glu Gln Leu Gln
7535 7540 7545

Asn Leu Asn Ser Leu Thr Asn Gly Gln Lys Asp Thr Ile Leu Asn
7550 7555 7560

His Ile Phe Ser Ala Pro Thr Arg Ser Gln Val Gly Glu Lys Ile
7565 7570 7575

Ala Ser Ala Lys Gln Leu Asn Asn Thr Met Lys Ala Leu Arg Asp
7580 7585 7590

Ser Ile Ala Asp Asn Asn Glu Ile Leu Gln Ser Ser Lys Tyr Phe
7595 7600 7605

Asn Glu Asp Ser Glu Gln Gln Asn Ala Tyr Asn Gln Ala Val Asn
7610 7615 7620

Lys Ala Lys Asn Ile Ile Asn Asp Gln Pro Thr Pro Val Met Ala
7625 7630 7635

Asn Asp Glu Ile Gln Ser Val Leu Asn Glu Val Lys Gln Thr Lys
7640 7645 7650

Asp Asn Leu His Gly Asp Gln Lys Leu Ala Asn Asp Lys Thr Asp
7655 7660 7665

Ala Gln Ala Thr Leu Asn Ala Leu Asn Tyr Leu Asn Gln Ala Gln
7670 7675 7680

Arg Gly Asn Leu Glu Thr Lys Val Gln Asn Ser Asn Ser Arg Pro
7685 7690 7695

Glu Val Gln Lys Val Val Gln Leu Ala Asn Gln Leu Asn Asp Ala
7700 7705 7710

P07741US01_6-19-06_Sequence.txt

Met Lys Lys Leu Asp Asp Ala Leu Thr Gly Asn Asp Ala Ile Lys
7715 7720 7725

Gln Thr Ser Asn Tyr Ile Asn Glu Asp Thr Ser Gln Gln Val Asn
7730 7735 7740

Phe Asp Glu Tyr Thr Asp Arg Gly Lys Asn Ile Val Ala Glu Gln
7745 7750 7755

Thr Asn Pro Asn Met Ser Pro Thr Asn Ile Asn Thr Ile Ala Asp
7760 7765 7770

Lys Ile Thr Glu Ala Lys Asn Asp Leu His Gly Val Gln Lys Leu
7775 7780 7785

Lys Gln Ala Gln Gln Ser Ile Asn Thr Ile Asn Gln Met Thr
7790 7795 7800

Gly Leu Asn Gln Ala Gln Lys Glu Gln Leu Asn Gln Glu Ile Gln
7805 7810 7815

Gln Thr Gln Thr Arg Ser Glu Val His Gln Val Ile Asn Lys Ala
7820 7825 7830

Gln Ala Leu Asn Asp Ser Met Asn Thr Leu Arg Gln Ser Ile Thr
7835 7840 7845

Asp Glu His Glu Val Lys Gln Thr Ser Asn Tyr Ile Asn Glu Thr
7850 7855 7860

Val Gly Asn Gln Thr Ala Tyr Asn Asn Ala Val Asp Arg Val Lys
7865 7870 7875

Gln Ile Ile Asn Gln Thr Ser Asn Pro Thr Met Asn Pro Leu Glu
7880 7885 7890

Val Glu Arg Ala Thr Ser Asn Val Lys Ile Ser Lys Asp Ala Leu
7895 7900 7905

P07741US01_6-19-06_Sequence.txt

His Gly Glu Arg Glu Leu Asn Asp Asn Lys Asn Ser Lys Thr Phe
7910 7915 7920

Ala val Asn His Leu Asp Asn Leu Asn Gln Ala Gln Lys Glu Ala
7925 7930 7935

Leu Thr His Glu Ile Glu Gln Ala Thr Ile Val Ser Gln Val Asn
7940 7945 7950

Asn Ile Tyr Asn Lys Ala Lys Ala Leu Asn Asn Asp Met Lys Lys
7955 7960 7965

Leu Lys Asp Ile Val Ala Gln Gln Asp Asn Val Arg Gln Ser Asn
7970 7975 7980

Asn Tyr Ile Asn Glu Asp Ser Thr Pro Gln Asn Met Tyr Asn Asp
7985 7990 7995

Thr Ile Asn His Ala Gln Ser Ile Ile Asp Gln Val Ala Asn Pro
8000 8005 8010

Thr Met Ser His Asp Glu Ile Glu Asn Ala Ile Asn Asn Ile Lys
8015 8020 8025

His Ala Ile Asn Ala Leu Asp Gly Glu His Lys Leu Gln Gln Ala
8030 8035 8040

Lys Glu Asn Ala Asn Leu Leu Ile Asn Ser Leu Asn Asp Leu Asn
8045 8050 8055

Ala Pro Gln Arg Asp Ala Ile Asn Arg Leu Val Asn Glu Ala Gln
8060 8065 8070

Thr Arg Glu Lys Val Ala Glu Gln Leu Gln Ser Ala Gln Ala Leu
8075 8080 8085

Asn Asp Ala Met Lys His Leu Arg Asn Ser Ile Gln Asn Gln Ser
8090 8095 8100

P07741US01_6-19-06_Sequence.txt

Ser Val Arg Gln Glu Ser Lys Tyr Ile Asn Ala Ser Asp Ala Lys
8105 8110 8115

Lys Glu Gln Tyr Asn His Ala Val Arg Glu Val Glu Asn Ile Ile
8120 8125 8130

Asn Glu Gln His Pro Thr Leu Asp Lys Glu Ile Ile Lys Gln Leu
8135 8140 8145

Thr Asp Gly Val Asn Gln Ala Asn Asn Asp Leu Asn Gly Val Glu
8150 8155 8160

Leu Leu Asp Ala Asp Lys Gln Asn Ala His Gln Ser Ile Pro Thr
8165 8170 8175

Leu Met His Leu Asn Gln Ala Gln Gln Asn Ala Leu Asn Glu Lys
8180 8185 8190

Ile Asn Asn Ala Val Thr Arg Thr Glu Val Ala Ala Ile Ile Gly
8195 8200 8205

Gln Ala Lys Leu Leu Asp His Ala Met Glu Asn Leu Glu Glu Ser
8210 8215 8220

Ile Lys Asp Lys Glu Gln Val Lys Gln Ser Ser Asn Tyr Ile Asn
8225 8230 8235

Glu Asp Ser Asp Val Gln Glu Thr Tyr Asp Asn Ala Val Asp His
8240 8245 8250

Val Thr Glu Ile Leu Asn Gln Thr Val Asn Pro Thr Leu Ser Ile
8255 8260 8265

Glu Asp Ile Glu His Ala Ile Asn Glu Val Asn Gln Ala Lys Lys
8270 8275 8280

Gln Leu Arg Gly Lys Gln Lys Leu Tyr Gln Thr Ile Asp Leu Ala
8285 8290 8295

P07741US01_6-19-06_Sequence.txt

Asp Lys Glu Leu Ser Lys Leu Asp Asp Leu Thr Ser Gln Gln Ser
8300 8305 8310

Ser Ser Ile Ser Asn Gln Ile Tyr Thr Ala Lys Thr Arg Thr Glu
8315 8320 8325

Val Ala Gln Ala Ile Glu Lys Ala Lys Ser Leu Asn His Ala Met
8330 8335 8340

Lys Ala Leu Asn Lys Val Tyr Lys Asn Ala Asp Lys Val Leu Asp
8345 8350 8355

Ser Ser Arg Phe Ile Asn Glu Asp Gln Pro Glu Lys Lys Ala Tyr
8360 8365 8370

Gln Gln Ala Ile Asn His Val Asp Ser Ile Ile His Arg Gln Thr
8375 8380 8385

Asn Pro Glu Met Asp Pro Thr Val Ile Asn Ser Ile Thr His Glu
8390 8395 8400

Leu Glu Thr Ala Gln Asn Asn Leu His Gly Asp Gln Lys Leu Ala
8405 8410 8415

His Ala Gln Gln Asp Ala Ala Asn Val Ile Asn Gly Leu Ile His
8420 8425 8430

Leu Asn Val Ala Gln Arg Glu Val Met Ile Asn Thr Asn Thr Asn
8435 8440 8445

Ala Thr Thr Arg Glu Lys Val Ala Lys Asn Leu Asp Asn Ala Gln
8450 8455 8460

Ala Leu Asp Lys Ala Met Glu Thr Leu Gln Gln Val Val Ala His
8465 8470 8475

Lys Asn Asn Ile Leu Asn Asp Ser Lys Tyr Leu Asn Glu Asp Ser
8480 8485 8490

P07741US01_6-19-06_Sequence.txt

Lys Tyr Gln Gln Gln Tyr Asp Arg Val Ile Ala Asp Ala Glu Gln
8495 8500 8505

Leu Leu Asn Gln Thr Thr Asn Pro Thr Leu Glu Pro Tyr Lys Val
8510 8515 8520

Asp Ile Val Lys Asp Asn Val Leu Ala Asn Glu Lys Ile Leu Phe
8525 8530 8535

Gly Ala Glu Lys Leu Ser Tyr Asp Lys Ser Asn Ala Asn Asp Glu
8540 8545 8550

Ile Lys His Met Asn Tyr Leu Asn Asn Ala Gln Lys Gln Ser Ile
8555 8560 8565

Lys Asp Met Ile Ser His Ala Ala Leu Arg Thr Glu Val Lys Gln
8570 8575 8580

Leu Leu Gln Gln Ala Lys Ile Leu Asp Glu Ala Met Lys Ser Leu
8585 8590 8595

Glu Asp Lys Thr Gln Val Val Ile Thr Asp Thr Thr Leu Pro Asn
8600 8605 8610

Tyr Thr Glu Ala Ser Glu Asp Lys Lys Glu Lys Val Asp Gln Thr
8615 8620 8625

Val Ser His Ala Gln Ala Ile Ile Asp Lys Ile Asn Gly Ser Asn
8630 8635 8640

Val Ser Leu Asp Gln Val Arg Gln Ala Leu Glu Gln Leu Thr Gln
8645 8650 8655

Ala Ser Glu Asn Leu Asp Gly Asp Gln Arg Val Glu Glu Ala Lys
8660 8665 8670

Val His Ala Asn Gln Thr Ile Asp Gln Leu Thr His Leu Asn Ser
8675 8680 8685

P07741US01_6-19-06_Sequence.txt

Leu Gln Gln Gln Thr Ala Lys Glu Ser Val Lys Asn Ala Thr Lys
8690 8695 8700

Leu Glu Glu Ile Ala Thr Val Ser Asn Asn Ala Gln Ala Leu Asn
8705 8710 8715

Lys Val Met Gly Lys Leu Glu Gln Phe Ile Asn His Ala Asp Ser
8720 8725 8730

Val Glu Asn Ser Asp Asn Tyr Arg Gln Ala Asp Asp Asp Lys Ile
8735 8740 8745

Ile Ala Tyr Asp Glu Ala Leu Glu His Gly Gln Asp Ile Gln Lys
8750 8755 8760

Thr Asn Ala Thr Gln Asn Glu Thr Lys Gln Ala Leu Gln Gln Leu
8765 8770 8775

Ile Tyr Ala Glu Thr Ser Leu Asn Gly Phe Glu Arg Leu Asn His
8780 8785 8790

Ala Arg Pro Arg Ala Leu Glu Tyr Ile Lys Ser Leu Glu Lys Ile
8795 8800 8805

Asn Asn Ala Gln Lys Ser Ala Leu Glu Asp Lys Val Thr Gln Ser
8810 8815 8820

His Asp Leu Leu Glu Leu Glu His Ile Val Asn Glu Gly Thr Asn
8825 8830 8835

Leu Asn Asp Ile Met Gly Glu Leu Ala Asn Ala Ile Val Asn Asn
8840 8845 8850

Tyr Ala Pro Thr Lys Ala Ser Ile Asn Tyr Ile Asn Ala Asp Asn
8855 8860 8865

Leu Arg Lys Asp Asn Phe Thr Gln Ala Ile Asn Asn Ala Arg Asp
8870 8875 8880

P07741US01_6-19-06_Sequence.txt

Ala Leu Asn Lys Thr Gln Gly Gln Asn Leu Asp Phe Asn Ala Ile
8885 8890 8895

Asp Thr Phe Lys Asp Asp Ile Phe Lys Thr Lys Asp Ala Leu Asn
8900 8905 8910

Gly Ile Glu Arg Leu Thr Ala Ala Lys Ser Lys Ala Glu Lys Leu
8915 8920 8925

Ile Asp Ser Leu Lys Phe Ile Asn Lys Ala Gln Phe Thr His Ala
8930 8935 8940

Asn Asp Glu Ile Ile Asn Thr Asn Ser Ile Ala Gln Leu Ser Arg
8945 8950 8955

Ile Val Asn Gln Ala Phe Asp Leu Asn Asp Ala Met Lys Ser Leu
8960 8965 8970

Arg Asp Glu Leu Asn Asn Gln Ala Phe Pro Val Gln Ala Ser Ser
8975 8980 8985

Asn Tyr Ile Asn Ser Asp Glu Asp Leu Lys Gln Gln Phe Asp His
8990 8995 9000

Ala Leu Ser Asn Ala Arg Lys Val Leu Ala Lys Glu Asn Gly Lys
9005 9010 9015

Asn Leu Asp Glu Lys Gln Ile Gln Gly Leu Lys Gln Val Ile Glu
9020 9025 9030

Asp Thr Lys Asp Ala Leu Asn Gly Ile Gln Arg Leu Ser Lys Ala
9035 9040 9045

Lys Ala Lys Ala Ile Gln Tyr Val Gln Ser Leu Ser Tyr Ile Asn
9050 9055 9060

Asp Ala Gln Arg His Ile Ala Glu Asn Asn Ile His Asn Ser Asp
9065 9070 9075

P07741US01_6-19-06_Sequence.txt

Asp Leu Ser Ser Leu Ala Asn Thr Leu Ser Lys Ala Ser Asp Leu
9080 9085 9090

Asp Asn Ala Met Lys Asp Leu Arg Asp Thr Ile Glu Ser Asn Ser
9095 9100 9105

Thr Ser Val Pro Asn Ser Val Asn Tyr Ile Asn Ala Asp Lys Asn
9110 9115 9120

Leu Gln Ile Glu Phe Asp Glu Ala Leu Gln Gln Ala Ser Ala Thr
9125 9130 9135

Ser Ser Lys Thr Ser Glu Asn Pro Ala Thr Ile Glu Glu Val Leu
9140 9145 9150

Gly Leu Ser Gln Ala Ile Tyr Asp Thr Lys Asn Ala Leu Asn Gly
9155 9160 9165

Glu Gln Arg Leu Ala Thr Glu Lys Ser Lys Asp Leu Lys Leu Ile
9170 9175 9180

Lys Gly Leu Lys Asp Leu Asn Lys Ala Gln Leu Glu Asp Val Thr
9185 9190 9195

Asn Lys Val Asn Ser Ala Asn Thr Leu Thr Glu Leu Ser Gln Leu
9200 9205 9210

Thr Gln Ser Thr Leu Glu Leu Asn Asp Lys Met Lys Leu Leu Arg
9215 9220 9225

Asp Lys Leu Lys Thr Leu Val Asn Pro Val Lys Ala Ser Leu Asn
9230 9235 9240

Tyr Arg Asn Ala Asp Tyr Asn Leu Lys Arg Gln Phe Asn Lys Ala
9245 9250 9255

Leu Lys Glu Ala Lys Gly Val Leu Asn Lys Asn Ser Gly Thr Asn
9260 9265 9270

P07741US01_6-19-06_Sequence.txt

Val Asn Ile Asn Asp Ile Gln His Leu Leu Thr Gln Ile Asp Asn
9275 9280 9285

Ala Lys Asp Gln Leu Asn Gly Glu Arg Arg Leu Lys Glu His Gln
9290 9295 9300

Gln Lys Ser Glu Val Phe Ile Ile Lys Glu Leu Asp Ile Leu Asn
9305 9310 9315

Asn Ala Gln Lys Ala Ala Ile Ile Asn Gln Ile Arg Ala Ser Lys
9320 9325 9330

Asp Ile Lys Ile Ile Asn Gln Ile Val Asp Asn Ala Ile Glu Leu
9335 9340 9345

Asn Asp Ala Met Gln Gly Leu Lys Glu His Val Ala Gln Leu Thr
9350 9355 9360

Ala Thr Thr Lys Asp Asn Ile Glu Tyr Leu Asn Ala Asp Glu Asp
9365 9370 9375

His Lys Leu Gln Tyr Asp Tyr Ala Ile Asn Leu Ala Asn Asn Val
9380 9385 9390

Leu Asp Lys Glu Asn Gly Thr Asn Lys Asp Ala Asn Ile Ile Ile
9395 9400 9405

Gly Met Ile Gln Asn Met Asp Asp Ala Arg Ala Leu Leu Asn Gly
9410 9415 9420

Ile Glu Arg Leu Lys Asp Ala Gln Thr Lys Ala His Asn Asp Ile
9425 9430 9435

Lys Asp Thr Leu Lys Arg Gln Leu Asp Glu Ile Glu His Ala Asn
9440 9445 9450

Ala Thr Ser Asn Ser Lys Ala Gln Ala Lys Gln Met Val Asn Glu
9455 9460 9465

P07741US01_6-19-06_Sequence.txt

Glu Ala Arg Lys Ala Leu Ser Asn Ile Asn Asp Ala Thr Ser Asn
9470 9475 9480

Asp Leu Val Asn Gln Ala Lys Asp Glu Gly Gln Ser Ala Ile Glu
9485 9490 9495

His Ile His Ala Asp Glu Leu Pro Lys Ala Lys Leu Asp Ala Asn
9500 9505 9510

Gln Met Ile Asp Gln Lys Val Glu Asp Ile Asn His Leu Ile Ser
9515 9520 9525

Gln Asn Pro Asn Leu Ser Asn Glu Glu Lys Asn Lys Leu Ile Ser
9530 9535 9540

Gln Ile Asn Lys Leu Val Asn Gly Ile Lys Asn Glu Ile Gln Gln
9545 9550 9555

Ala Ile Asn Lys Gln Gln Ile Glu Asn Ala Thr Thr Lys Leu Asp
9560 9565 9570

Glu Val Ile Glu Thr Thr Lys Lys Leu Ile Ile Ala Lys Ala Glu
9575 9580 9585

Ala Lys Gln Met Ile Lys Glu Leu Ser Gln Lys Lys Arg Asp Ala
9590 9595 9600

Ile Asn Asn Asn Thr Asp Leu Thr Pro Ser Gln Lys Ala His Ala
9605 9610 9615

Leu Ala Asp Ile Asp Lys Thr Glu Lys Asp Ala Leu Gln His Ile
9620 9625 9630

Glu Asn Ser Asn Ser Ile Asp Asp Ile Asn Asn Asn Lys Glu His
9635 9640 9645

Ala Phe Asn Thr Leu Ala His Ile Ile Ile Trp Asp Thr Asp Gln
9650 9655 9660

P07741US01_6-19-06_Sequence.txt

Gln Pro Leu Val Phe Glu Leu Pro Glu Leu Ser Leu Gln Asn Ala
9665 9670 9675

Leu Val Thr Ser Glu Val Val Val His Arg Asp Glu Thr Ile Ser
9680 9685 9690

Leu Glu Ser Ile Ile Gly Ala Met Thr Leu Thr Asp Glu Leu Lys
9695 9700 9705

Val Asn Ile Val Ser Leu Pro Asn Thr Asp Lys Val Ala Asp His
9710 9715 9720

Leu Thr Ala Lys Val Lys Val Ile Leu Ala Asp Gly Ser Tyr Val
9725 9730 9735

Thr Val Asn Val Pro Val Lys Val Val Glu Lys Glu Leu Gln Ile
9740 9745 9750

Ala Lys Lys Asp Ala Ile Lys Thr Ile Asp Val Leu Val Lys Gln
9755 9760 9765

Lys Ile Lys Asp Ile Asp Ser Asn Asn Glu Leu Thr Ser Thr Gln
9770 9775 9780

Arg Glu Asp Ala Lys Ala Glu Ile Glu Arg Leu Lys Lys Gln Ala
9785 9790 9795

Ile Asp Lys Val Asn His Ser Lys Ser Ile Lys Asp Ile Glu Thr
9800 9805 9810

Val Lys Arg Thr Asp Phe Glu Glu Ile Asp Gln Phe Asp Pro Lys
9815 9820 9825

Arg Phe Thr Leu Asn Lys Ala Lys Lys Asp Ile Ile Thr Asp Val
9830 9835 9840

Asn Thr Gln Ile Gln Asn Gly Phe Lys Glu Ile Glu Thr Ile Lys
9845 9850 9855

P07741US01_6-19-06_Sequence.txt

Gly Leu Thr Ser Asn Glu Lys Thr Gln Phe Asp Lys Gln Leu Thr
9860 9865 9870

Ala Leu Gln Lys Glu Phe Leu Glu Lys Val Glu His Ala His Asn
9875 9880 9885

Leu Val Glu Leu Asn Gln Leu Gln Gln Glu Phe Asn Asn Arg Tyr
9890 9895 9900

Lys His Ile Leu Asn Gln Ala His Leu Leu Gly Glu Lys His Ile
9905 9910 9915

Ala Glu His Lys Leu Gly Tyr Val Val Val Asn Lys Thr Gln Gln
9920 9925 9930

Ile Leu Asn Asn Gln Ser Ala Ser Tyr Phe Ile Lys Gln Trp Ala
9935 9940 9945

Leu Asp Arg Ile Lys Gln Ile Gln Leu Glu Thr Met Asn Ser Ile
9950 9955 9960

Arg Gly Ala His Thr Val Gln Asp Val His Lys Ala Leu Leu Gln
9965 9970 9975

Gly Ile Glu Gln Ile Leu Lys Val Asn Val Ser Ile Ile Asn Gln
9980 9985 9990

Ser Phe Asn Asp Ser Leu His Asn Phe Asn Tyr Leu His Ser Lys
9995 10000 10005

Phe Asp Ala Arg Leu Arg Glu Lys Asp Val Ala Asn His Ile Val
10010 10015 10020

Gln Thr Glu Thr Phe Lys Glu Val Leu Lys Gly Thr Gly Val Glu
10025 10030 10035

Pro Gly Lys Ile Asn Lys Glu Thr Gln Gln Pro Lys Leu His Lys
10040 10045 10050

P07741US01_6-19-06_Sequence.txt

Asn Asp Asn Asp Ser Leu Phe Lys His Leu Val Asp Asn Phe Gly
10055 10060 10065

Lys Thr Val Gly Val Ile Thr Leu Thr Gly Leu Leu Ser Ser Phe
10070 10075 10080

Trp Leu Val Leu Ala Lys Arg Arg Lys Lys Glu Glu Glu Glu Lys
10085 10090 10095

Gln Ser Ile Lys Asn His His Lys Asp Ile Arg Leu Ser Asp Thr
10100 10105 10110

Asp Lys Ile Asp Pro Ile Val Ile Thr Lys Arg Lys Ile Asp Lys
10115 10120 10125

Glu Glu Gln Ile Gln Asn Asp Asp Lys His Ser Ile Pro Val Ala
10130 10135 10140

Lys His Lys Lys Ser Lys Glu Lys Gln Leu Ser Glu Glu Asp Ile
10145 10150 10155

His Ser Ile Pro Val Val Lys Arg Lys Gln Asn Ser Asp Asn Lys
10160 10165 10170

Asp Thr Lys Gln Lys Lys Val Thr Ser Lys Lys Lys Lys Thr Pro
10175 10180 10185

Gln Ser Thr Lys Lys Val Val Lys Thr Lys Lys Arg Ser Lys Lys
10190 10195 10200

<210> 24
<211> 1973

<212> PRT

<213> Staphylococcus epidermidis

<400> 24

Met Lys Glu Asn Lys Arg Lys Asn Asn Leu Asp Lys Asn Asn Thr Arg
1 5 10 15

P07741US01_6-19-06_Sequence.txt

Phe Ser Ile Arg Lys Tyr Gln Gly Tyr Gly Ala Thr Ser Val Ala Ile
20 25 30

Ile Gly Phe Ile Ile Ser Cys Phe Ser Glu Ala Lys Ala Asp Ser
35 40 45

Asp Lys His Glu Ile Lys Ser His Gln Gln Ser Met Thr Asn His Leu
50 55 60

Thr Thr Leu Pro Ser Asp Asn Gln Glu Asn Thr Ser Asn Asn Glu Phe
65 70 75 80

Asn Asn Arg Asn His Asp Ile Ser His Leu Ser Leu Asn Lys Ser Ile
85 90 95

Gln Met Asp Glu Leu Lys Lys Leu Ile Lys Gln Tyr Lys Ala Ile Asn
100 105 110

Leu Asn Asp Lys Thr Glu Glu Ser Ile Lys Leu Phe Gln Ser Asp Leu
115 120 125

Val Gln Ala Glu Ser Leu Ile Asn Asn Pro Gln Ser Gln Gln His Val
130 135 140

Asp Ala Phe Tyr His Lys Phe Leu Asn Ser Ala Gly Lys Leu Arg Lys
145 150 155 160

Lys Glu Thr Val Ser Ile Lys His Glu Arg Ser Glu Ser Asn Thr Tyr
165 170 175

Arg Leu Gly Asp Glu Val Arg Ser Gln Thr Phe Ser His Ile Arg His
180 185 190

Lys Arg Asn Ala Val Ser Phe Arg Asn Ala Asp Gln Ser Asn Leu Ser
195 200 205

Thr Asp Pro Leu Lys Ala Asn Glu Ile Asn Pro Glu Ile Gln Asn Gly
210 215 220

P07741US01_6-19-06_Sequence.txt

Asn Phe Ser Gln Val Ser Gly Gly Pro Leu Pro Thr Ser Ser Lys Arg
225 230 235 240

Leu Thr Val Val Thr Asn Val Asp Asn Trp His Ser Tyr Ser Thr Asp
245 250 255

Pro Asn Pro Glu Tyr Pro Met Phe Tyr Thr Thr Ala Val Asn Tyr
260 265 270

Pro Asn Phe Met Ser Asn Gly Asn Ala Pro Tyr Gly Val Ile Leu Gly
275 280 285

Arg Thr Thr Asp Gly Trp Asn Arg Asn Val Ile Asp Ser Lys Val Ala
290 295 300

Gly Ile Tyr Gln Asp Ile Asp Val Val Pro Gly Ser Glu Leu Asn Val
305 310 315 320

Asn Phe Ile Ser Thr Ser Pro Val Phe Ser Asp Gly Ala Ala Gly Ala
325 330 335

Lys Leu Lys Ile Ser Asn Val Glu Gln Asn Arg Val Leu Phe Asp Ser
340 345 350

Arg Leu Asn Gly Met Gly Pro Tyr Pro Thr Gly Lys Leu Ser Ala Met
355 360 365

Val Asn Ile Pro Asn Asp Ile Asn Arg Val Arg Ile Ser Phe Leu Pro
370 375 380

Val Ser Ser Thr Gly Arg Val Ser Val Gln Arg Ser Ser Arg Glu His
385 390 395 400

Gly Phe Gly Asp Asn Ser Ser Tyr Tyr His Gly Gly Ser Val Ser Asp
405 410 415

Val Arg Ile Asn Ser Gly Ser Tyr Val Val Ser Lys Val Thr Gln Arg
420 425 430

P07741US01_6-19-06_Sequence.txt

Glu Tyr Thr Thr Arg Pro Asn Ser Ser Asn Asp Thr Phe Ala Arg Ala
435 440 445

Thr Ile Asn Leu Ser Val Glu Asn Lys Gly His Asn Gln Ser Lys Asp
450 455 460

Thr Tyr Tyr Glu Val Ile Leu Pro Gln Asn Ser Arg Leu Ile Ser Thr
465 470 475 480

Arg Gly Gly Ser Gly Asn Tyr Asn Asn Ala Thr Asn Lys Leu Ser Ile
485 490 495

Arg Leu Asp Asn Leu Asn Pro Gly Asp Arg Arg Asp Ile Ser Tyr Thr
500 505 510

Val Asp Phe Glu Ser Ser Ser Pro Lys Leu Ile Asn Leu Asn Ala His
515 520 525

Leu Leu Tyr Lys Thr Asn Ala Thr Phe Arg Gly Asn Asp Gly Gln Arg
530 535 540

Thr Gly Asp Asn Ile val Asp Leu Gln Ser Ile Ala Leu Leu Met Asn
545 550 555 560

Lys Asp Val Leu Glu Thr Glu Leu Asn Glu Ile Asp Lys Phe Ile Arg
565 570 575

Asp Leu Asn Glu Ala Asp Phe Thr Ile Asp Ser Trp Ser Ala Leu Gln
580 585 590

Glu Lys Met Thr Glu Gly Gly Asn Ile Leu Asn Glu Gln Gln Asn Gln
595 600 605

Val Ala Leu Glu Asn Gln Ala Ser Gln Glu Thr Ile Asn Asn Val Thr
610 615 620

Gln Ser Leu Glu Ile Leu Lys Asn Asn Leu Lys Tyr Lys Thr Pro Ser
625 630 635 640

P07741US01_6-19-06_Sequence.txt

Gln Pro Ile Ile Lys Ser Asn Asn Gln Ile Pro Asn Ile Thr Ile Ser
645 650 655

Pro Ala Asp Lys Ala Asp Lys Leu Thr Ile Thr Tyr Gln Asn Thr Asp
660 665 670

Asn Glu Ser Ala Ser Ile Ile Gly Asn Lys Leu Asn Asn Gln Trp Ser
675 680 685

Leu Asn Asn Asn Ile Pro Gly Ile Glu Ile Asp Met Gln Thr Gly Leu
690 695 700

Val Thr Ile Asp Tyr Lys Ala Val Tyr Pro Glu Ser Val Val Gly Ala
705 710 715 720

Asn Asp Lys Thr Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr
725 730 735

Met Pro Arg Lys Glu Ala Thr Pro Leu Ser Pro Ile Val Glu Ala Asn
740 745 750

Glu Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln
755 760 765

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu Val
770 775 780

Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile Asp Tyr
785 790 795 800

Val Asn Ile Glu Glu Asn Ser Gly Lys Val Thr Ile Gly Tyr Gln Ala
805 810 815

Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr Lys Gly Asn Ser
820 825 830

Asp Glu Ser Ala Glu Ser Arg Val Thr Met Pro Arg Lys Glu Ala Thr
835 840 845

P07741US01_6-19-06_Sequence.txt

Pro His Ser Pro Ile Val Glu Ala Asn Glu Glu His Val Asn Val Thr
850 855 860

Ile Ala Pro Asn Gly Glu Ala Thr Gln Ile Ala Ile Lys Tyr Arg Thr
865 870 875 880

Pro Asp Gly Gln Glu Thr Thr Leu Ile Ala Ser Lys Asn Gly Ser Ser
885 890 895

Trp Thr Leu Asn Lys Gln Ile Asp Tyr Val Asn Ile Glu Glu Asn Ser
900 905 910

Gly Lys Val Thr Ile Gly Tyr Gln Ala Val Gln Leu Glu Ser Glu Val
915 920 925

Ile Ala Thr Glu Thr Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg
930 935 940

Ile Thr Met Leu Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu
945 950 955 960

Ala Asn Glu Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Ala
965 970 975

Thr Gln Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr
980 985 990

Leu Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
995 1000 1005

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1010 1015 1020

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr
1025 1030 1035

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1040 1045 1050

P07741US01_6-19-06_Sequence.txt

Arg Lys Glu Ala Thr Pro Ile Pro Pro Thr Leu Glu Ala Ser Val
1055 1060 1065

Gln Glu Ala Ser Val Thr Val Thr Pro Asn Glu Asn Ala Thr Lys
1070 1075 1080

Val Phe Ile Lys Tyr Leu Asp Ile Asn Asp Glu Ile Ser Thr Ile
1085 1090 1095

Ile Ala Ser Lys Ile Asn Gln Gln Trp Thr Leu Asn Lys Asp Asn
1100 1105 1110

Phe Gly Ile Lys Ile Asn Pro Leu Thr Gly Lys Val Ile Ile Ser
1115 1120 1125

Tyr Val Ala Val Gln Pro Glu Ser Asp Val Ile Ala Ile Glu Ser
1130 1135 1140

Gln Gly Asn Ser Asp Leu Ser Glu Glu Ser Arg Ile Ile Met Pro
1145 1150 1155

Thr Lys Glu Glu Pro Pro Glu Pro Pro Ile Leu Glu Ser Asp Ser
1160 1165 1170

Ile Glu Ala Lys Val Asn Ile Phe Pro Asn Asp Glu Ala Thr Arg
1175 1180 1185

Ile Val Ile Met Tyr Thr Ser Leu Glu Gly Gln Glu Ala Thr Leu
1190 1195 1200

Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
1205 1210 1215

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1220 1225 1230

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr
1235 1240 1245

P07741US01_6-19-06_Sequence.txt

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Val Thr Met Pro
1250 1255 1260

Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu Thr Asn Glu
1265 1270 1275

Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln
1280 1285 1290

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Thr Thr Leu
1295 1300 1305

Ile Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile
1310 1315 1320

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1325 1330 1335

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr
1340 1345 1350

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1355 1360 1365

Arg Lys Glu Ala Ile Pro His Ser Pro Ile Val Glu Ala Asn Glu
1370 1375 1380

Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Thr Thr Gln
1385 1390 1395

Ile Ala Val Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu
1400 1405 1410

Ile Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile
1415 1420 1425

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly
1430 1435 1440

P07741US01_6-19-06_Sequence.txt

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr
1445 1450 1455

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro
1460 1465 1470

Val Lys Glu Lys Thr Pro Ala Pro Pro Ile Ser Ile Ile Asn Glu
1475 1480 1485

Ser Asn Ala Ser Val Glu Ile Ile Pro Gln Val Asn Val Thr Gln
1490 1495 1500

Leu Ser Leu Gln Tyr Ile Asp Ala Lys Gly Gln Gln Gln Asn Leu
1505 1510 1515

Ile Ala Thr Leu Asn Gln Asn Gln Trp Thr Leu Asn Lys Asn Val
1520 1525 1530

Ser His Ile Thr Val Asp Lys Asn Thr Gly Lys Val Leu Ile Asn
1535 1540 1545

Tyr Gln Ala Val Tyr Pro Glu Ser Glu Val Ile Ala Arg Glu Ser
1550 1555 1560

Lys Gly Asn Ser Asp Ser Ser Asn Val Ser Met Val Ile Met Pro
1565 1570 1575

Arg Lys Thr Ala Thr Pro Lys Pro Pro Ile Ile Lys Val Asp Glu
1580 1585 1590

Met Asn Ala Ser Leu Ala Ile Ile Pro Tyr Lys Asn Asn Thr Ala
1595 1600 1605

Ile Asn Ile His Tyr Ile Asp Lys Lys Gly Ile Lys Ser Met Val
1610 1615 1620

Thr Ala Ile Lys Asn Asn Asp Gln Trp Gln Leu Asp Glu Lys Ile
1625 1630 1635

P07741US01_6-19-06_Sequence.txt

Lys Tyr Val Lys Ile Asp Ala Lys Thr Gly Thr Val Ile Ile Asn
1640 1645 1650

Tyr Gln Ile Val Gln Glu Asn Ser Glu Ile Ile Ala Thr Ala Ile
1655 1660 1665

Asn Gly Asn Ser Asp Lys Ser Glu Glu Val Lys Val Leu Met Pro
1670 1675 1680

Ile Lys Glu Phe Thr Pro Leu Ala Pro Leu Leu Glu Thr Asn Tyr
1685 1690 1695

Lys Lys Ala Thr Val Ser Ile Leu Pro Gln Ser Asn Ala Thr Lys
1700 1705 1710

Leu Asp Phe Lys Tyr Arg Asp Lys Lys Gly Asp Ser Lys Ile Ile
1715 1720 1725

Ile Val Lys Arg Phe Lys Asn Ile Trp Lys Ala Asn Glu Gln Ile
1730 1735 1740

Ser Gly Val Thr Ile Asn Pro Glu Phe Gly Gln Val Val Ile Asn
1745 1750 1755

Tyr Gln Ala Val Tyr Pro Glu Ser Asp Ile Leu Ala Ala Gln Tyr
1760 1765 1770

Val Gly Asn Ser Asp Ala Ser Glu Trp Ala Lys Val Lys Met Pro
1775 1780 1785

Lys Lys Glu Leu Ala Pro His Ser Pro Ser Leu Ile Tyr Asp Asn
1790 1795 1800

Arg Asn Asn Lys Ile Leu Ile Ala Pro Asn Ser Asn Ala Thr Glu
1805 1810 1815

Met Glu Leu Ser Tyr Val Asp Lys Asn Asn Gln Ser Leu Lys Val
1820 1825 1830

P07741US01_6-19-06_Sequence.txt

Lys Ala Leu Lys Ile Asn Asn Arg Trp Lys Phe Asp Ser Ser Val
1835 1840 1845

Ser Asn Ile Ser Ile Asn Pro Asn Thr Gly Lys Ile Val Leu Gln
1850 1855 1860

Pro Gln Phe Leu Leu Thr Asn Ser Lys Ile Ile Val Phe Ala Lys
1865 1870 1875

Lys Gly Asn Ser Asp Ala Ser Ile Ser Val Ser Leu Arg Val Pro
1880 1885 1890

Ala Val Lys Lys Ile Glu Leu Glu Pro Met Phe Asn Val Pro Val
1895 1900 1905

Leu Val Ser Leu Asn Lys Lys Arg Ile Gln Phe Asp Asp Cys Ser
1910 1915 1920

Gly Val Lys Asn Cys Leu Asn Lys Gln Ile Ser Lys Thr Gln Leu
1925 1930 1935

Pro Asp Thr Gly Tyr Ser Asp Lys Ala Ser Lys Ser Asn Ile Leu
1940 1945 1950

Ser Val Leu Leu Leu Gly Phe Gly Phe Leu Ser Tyr Ser Arg Lys
1955 1960 1965

Arg Lys Glu Lys Gln
1970

<210> 25
<211> 10
<212> PRT
<213> Enterococcus faecalis

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

P07741US01_6-19-06_Sequence.txt

<400> 25

Leu Pro Xaa Thr Ser Ala Gly Ala Asn Ser
1 5 10

<210> 26

<211> 30

<212> DNA

<213> Enterococcus faecalis

<400> 26

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30

<210> 27

<211> 33

<212> DNA

<213> Enterococcus faecalis

<400> 27

ccgtcgactt aagtaccaga agtggtggtt ttc
33

<210> 28

<211> 30

<212> DNA

<213> Enterococcus faecalis

<400> 28

ccgcatgcc aagcaaca gcaaaagaag
30

<210> 29

<211> 33

<212> DNA

<213> Enterococcus faecalis

<400> 29

gggtcgactt attgttcaa gtttacttct gtc
33

<210> 30

<211> 33

<212> DNA

<213> Enterococcus faecalis

<400> 30

P07741US01_6-19-06_Sequence.txt

ccggatccgc agctaataaa gaagaatttt tag
33

<210> 31
<211> 33
<212> DNA
<213> Enterococcus faecalis

<400> 31
ccgtcgactt aagtaccaga agtggtggtt ttc
33

<210> 32
<211> 28
<212> DNA
<213> Enterococcus faecalis

<400> 32
ccgagctcga agaggtaac agcgatgg
28

<210> 33
<211> 31
<212> DNA
<213> Enterococcus faecalis

<400> 33
ccctgcagtt acccaccaaa tgtgataacc c
31

<210> 34
<211> 33
<212> DNA
<213> Enterococcus faecalis

<400> 34
ccggatccga agaaataact gatttatttt tac
33

<210> 35
<211> 36
<212> DNA
<213> Enterococcus faecalis

<400> 35
ccgagctctt attgttcctg aattaatttt tctaac
36

P07741US01_6-19-06_Sequence.txt

<210> 36
<211> 27
<212> DNA
<213> Enterococcus faecalis

<400> 36
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27

<210> 37
<211> 33
<212> DNA
<213> Enterococcus faecalis

<400> 37
ccctgcagtt agaaggctga ctctttact ttt
33

<210> 38
<211> 30
<212> DNA
<213> Enterococcus faecalis

<400> 38
ccggatccca agaagtaaca agtgatgctg
30

<210> 39
<211> 32
<212> DNA
<213> Enterococcus faecalis

<400> 39
ccgagctt aagttacttg ttcgtccgca at
32

<210> 40
<211> 28
<212> DNA
<213> Enterococcus faecalis

<400> 40
ccggatccga aacaggatat gcgcaaac
28

P07741US01_6-19-06_Sequence.txt

<210> 41
<211> 32
<212> DNA
<213> Enterococcus faecalis

<400> 41
ccgagctctt attccttatt acgaatcgcc tg
32

<210> 42
<211> 29
<212> DNA
<213> Enterococcus faecalis

<400> 42
gcgggatccg aagaaaatgg ggagagcgc
29

<210> 43
<211> 33
<212> DNA
<213> Enterococcus faecalis

<400> 43
gcggagctct taggtacctt tgtgtttgtt tgg
33

<210> 44
<211> 22
<212> DNA
<213> Enterococcus faecalis

<400> 44
gaattgagca aaagttcaat cg
22

<210> 45
<211> 22
<212> DNA
<213> Enterococcus faecalis

<400> 45
caagtaaaaa agccggtaca gc
22

<210> 46
<211> 19

P07741US01_6-19-06_Sequence.txt

<212> DNA
<213> Enterococcus faecalis

<400> 46
tcgcaagcaa gcgttcaag
19

<210> 47
<211> 18
<212> DNA
<213> Enterococcus faecalis

<400> 47
gagagcgcac agctcgta
18

<210> 48
<211> 34
<212> DNA
<213> Enterococcus faecalis

<400> 48
cgggatccca aaacagcgaa aaagaaatga gcga
34

<210> 49
<211> 32
<212> DNA
<213> Enterococcus faecalis

<400> 49
cgggatccga aatggttcag attactttac ac
32

<210> 50
<211> 35
<212> DNA
<213> Enterococcus faecalis

<400> 50
cgggatccaa agcactgaac atcaagctaa atgcg
35

<210> 51
<211> 26
<212> DNA
<213> Enterococcus faecalis

P07741US01_6-19-06_Sequence.txt

<400> 51
gtctgtcttt tcacttgttt ctgttg
26

<210> 52
<211> 21
<212> DNA
<213> Enterococcus faecalis

<400> 52
aaaggaacct ttgcttggtt c
21

<210> 53
<211> 27
<212> DNA
<213> Enterococcus faecalis

<400> 53
aagcctgact ctttacttt tttattg
27

<210> 54
<211> 24
<212> DNA
<213> Enterococcus faecalis

<400> 54
ggtaccttg tgtttgttg gtac
24

<210> 55
<211> 33
<212> DNA
<213> Enterococcus faecalis

<400> 55
cccaagctt catgtacctt tgtgtttatt tgg
33

<210> 56
<211> 35
<212> DNA
<213> Enterococcus faecalis

<400> 56

P07741US01_6-19-06_Sequence.txt

tctgcagttc aattgactac tttcaatata ctgtc
35

<210> 57
<211> 36
<212> DNA
<213> Enterococcus faecalis

<400> 57
cccaagctt cagaatgctt gaccttgatt attgta
36